

## NUCLEIC ACID SEQUENCE

GTGACCCACGCGTCCGGCCCTGGAGAAAGGAAGAACTTATAATAAATG  
GGAAATTATAAATCTAGACCAACCCAAACTTGTACTGATGAATGGAAGAA  
AAAAGTCAGTGAATCATATGTTATCACAATAGAAAGATTAGAAGATGACC  
TGCAGATCAAGGAAAAAGAACTGACAGAACTAAGGAATATATTTGGCTCT  
GATGAAGCCTTCAGTAAAGTCAATTTAAATTACCGCACTGAAAATGGGCT  
GTCTCTACTTCATTTATGTTGCATTTGTGGAGGCAAGAAATCACATATTC  
GAACCTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAATGGA  
TTTACAGCCTTGCATTTAGCAGTTTACAAGGATAATGCAGAATTGATCAC  
TTCTCTGCTTCACAGTGGAGCTGATATACAGCAGGTTGGATACGGTGGCC  
TCACTGCCCTCCATATTGCTACAATAGCTGGCCACCTAGAGGCTGCTGAT  
GTGCTGTTGCAACATGGAGCTAATGTCAATATTCAAGATGCAGTTTTTTT  
CACTCCATTGCATATTGCAGCGTACTATGGACATGAACAGGTAACCTCGCC  
TTCTTTTGAATTTGGTGCTGATGTAAATGTAAGTGGTGAAGTTGGAGAT  
AGACCCCTCCACCTAGCATCTGCAAAAGGATTCTTGAATATTGCAAACT  
CTTGATGGAAGGAGGCAGCAAGCAGATGTGAATGCTCAAGATAAGAG  
ACCATGTCCCACTCCATTTCTGTTCTCGATTTGGACACCATGATATAGTT  
AAGTATCTGCTGCAAGTGATTTGGAAGTTCAACCTCATGTTGTTAATAT  
CTATGGAGATACCCCTTACACCTGGCATGCTACAATGGCAAATTTGAAG  
TTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAGGAA  
AACATCTTCAGTGAAACAGCTTTTTCATAGTGCTTGTACCTATGGCAAGAG  
CATTGACCTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACC  
ACCAAGGAAGGGATGGGCACACTGGATTACACTCTGCTTGCTACCACGGT  
CACATTCGCCTGGTTCAGTTCCTTACTGGATAAATGGAGCTGATATGAATCT  
AGTGGCTTGTGATCCCAGCAGGTCTAGTGGTGAAAAAGATGAGCAGACAT  
GTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTACACTCCTG  
AAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCA  
GCCTGGAGGAGATGGCTCCTATGTGTCTGTTCCATCACCCCTTGGGGAAGA  
TTAAAGCATGACAAAAGAGAAGGCAGATATTCTCCTCCTAAGAGCTGGA  
TTGCCTTCACATTTCCATCTTCAGCTCTCAGAAATTGAGTTCATGAGAT  
TATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGACGATGCAGAAATA  
AAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAGTCA  
GATGTGGATATGTTTTGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCA  
TCCCTGCGTAATTCAAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGT  
TTGCCATTGTCACTCAATACATATCAGGGGGTCTCTGTTCTCCCTCCTT  
CATGAGCAGAAGAGGATTCTTGATTGTCAGTCTAAATTAATTATTGCAGT  
AGATGTTTGCCAAAGGCATGGAGTACCTTCACAACCTGACACAGCCAATTA  
TACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGGCAT  
GCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGA  
AGACAACATGACAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGG  
TGTTACAGCAGTGCACCTCGGTACACCATCAAAGCAGATGTCTTCAGCTAT  
GCTCTGTGTCTGTGGGAAATTCCTCACTGGCGAAATTCATTCGCTCATCT  
CAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCACCACATCAGACCTC  
CCATTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGAGGG  
TGGAACGCATGTCCTGAAGGAAGACCCGAATTTTCTGAAGTTGTCATGAA  
GTTAGAAGAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTA  
ACAGCAGTGGGTCTCTCTCACCTTCTTCTTCTGATTGCCTGGTGAAC  
CGGGGAGGACCTGGCCGGAGTTCATGTGGCAGCATTAAGAAGTCGTTTCGA  
ATTGGAATATGCTCTAAATGCAAGGTCCATGCTGCTTTGTCCCAAAGTG  
CTGGACAATATTCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGAAGT  
CTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAG  
CTCAATGCATTTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCA  
GCTGACAGCATTCGGCGTATACCTAAGGAGAGTTTTTTTCCCCGAAGTAC  
AGCAACGATTCCAACCACGGCAAGCTGGCTTCCAACCTATAACATTTTACT  
CTCAAAGGTCTCCTTAAATGGGCTTGTTTTTACTTGTCTATTTAATTC

Fig. 1A

CCCACTATTAGCAGGCTTTGGATTTGTGCCTAAGGAATAATATGCAAAAG  
AACCAAGACAGAATGTATATGAAGAATTGTTTTTAATTTGTAAATTAAA  
AAAAAATTTAGATCGTTACTTGGAAATGGAGCCTAAGTCTGTGGTGGACA  
GATAATAATTATGTTTTCTTGGGCTGAATTATGTAGACTTGTGTTTGACA  
GCTATGGGTTTATTTCTTAGAACATTGTTTCAATTTCTTTCTCATTATGT  
TACTTCTAGTGTTACCTCTGTGATTAAAGATTCTTTGGTGAAATAGAAA  
AAAAAAAAAAAAAAAAAGGGCGGCCGC

#### AMINO ACID SEQUENCE

MGNYKS RPTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTEL RNIFGSDEAFSKVNL  
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL  
LHSGADIQQVGYGGLTALHIATIAAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAAYYGHE  
QVTRLLLKFGADVNVSGEVDRLPLHLASAKGFLNIAKLLMEEGSKADVNAQDVEDHVPLH  
FCSRFGHHDIVKYLLQSDLEVQPHVVNIYGDTPHLACYNKGFEVAKETIIQISGTESLTK  
ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQGRDGHTGLHSACYHGHIRLVQFLL  
DNGADMNLVACDPSRSSGEKDEQTC LMWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG  
GDGSYVSVPSPLGKIKSMTKEKADILLRAGLP SHFHLQLSEIEFHEIIGSGSFGKVYKG  
RCRNKIVAIAKRYRANTYCSKSDVDMFCREVSILCQLNHPCV IQFVGACLN DPSQFAIVTQ  
YISGGSLSFSLHEQKRILDLSKLIIAVDVAKGMEYLHNLTPQIIHRDLNSHNILLYEDG  
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT  
GEIPFAHLKPAAAAAD MAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE  
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA  
LSQSAGQYSSQGLSLEEMKRSLO YTPIDKYGYVSDPMSSMHFHS CRNSSSFEDS

Fig. 1B

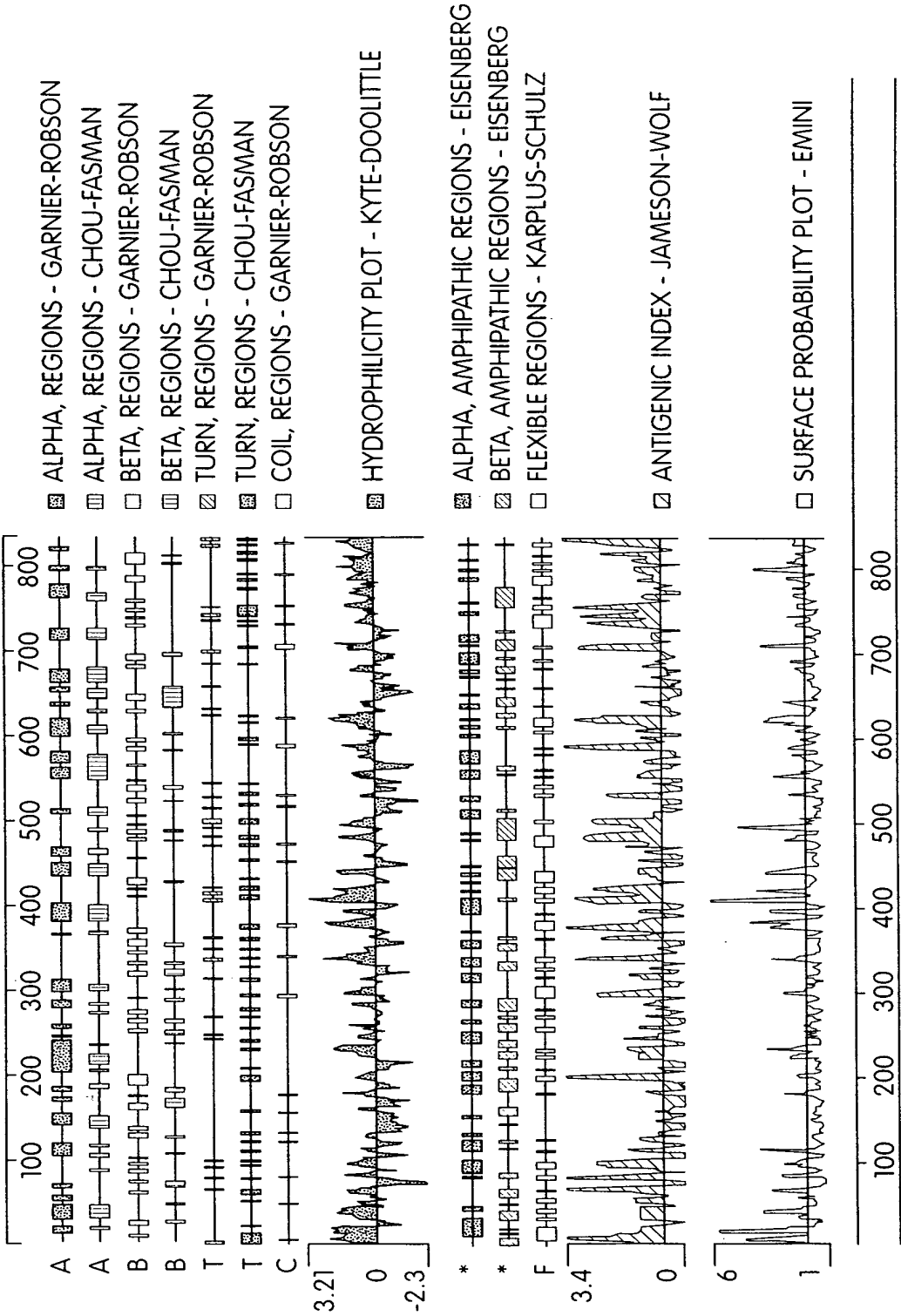


Fig. 2

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M E E I - - - - - E W - K T - S - - - - -																												Majority										
10														20														30										
1	M	G	N	Y	K	S	R	P	T	Q	T	C	T	D	E	W	K	K	V	S	E	S	Y	V	I	T	I	E	R	CARP2/prot								
1	M	E	K	K	-	-	-	-	-	-	-	-	-	S	E	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2							
1	M	S	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3							
1	M	S	C	S	S	S	S	G	S	E	G	E	E	E	G	F	D	A	-	-	-	-	-	-	-	-	-	-	-	-	Arabidopsis thaliana							
1	M	R	T	F	-	-	-	-	-	-	-	-	-	S	D	E	L	K	K	K	I	S	E	G	Y	S	V	V	R	S	R	c.elegans kinase						
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)							
1	G	T	E	T	-	-	-	-	-	-	-	-	-	T	-	-	-	-	R	M	E	E	D	-	Q	I	S	C	-	S	D.Discoideum (U01064)							
1	M	E	E	E	E	G	-	-	-	-	-	-	-	A	V	A	K	E	W	G	T	T	P	A	G	P	V	W	T	A	V	F	D	H.sapiens (Z48615)				
1	M	E	E	E	E	G	-	-	-	-	-	-	-	A	V	A	K	E	W	G	T	T	P	A	G	P	V	W	T	A	V	F	D	Homo sapiens (Z48615)				
1	M	E	H	I	Q	G	-	-	-	-	-	-	-	-	A	W	-	K	T	I	S	N	G	F	-	-	-	-	-	-	-	-	Human raf1(W13107)					
1	M	E	H	I	Q	G	-	-	-	-	-	-	-	-	A	W	-	K	T	I	S	N	G	F	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)					
1	M	G	E	D	-	-	-	-	-	-	-	-	-	G	N	S	W	I	R	R	T	N	F	S	-	H	T	V	C	H	R	Soybean kinase(M67449)						
- - - - - L - - - - -																												Majority										
40														50														60										
31	L	E	D	D	L	Q	I	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	K	E	L	T	E	L	R	N	CARP2/prot				
8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2					
6	F	N	-	-	-	-	P	F	R	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3					
19	-	-	-	-	-	-	-	-	-	-	Y	R	K	G	G	Y	H	A	V	R	I	G	D	P	F	S	G	G	R	Y	-	-	Arabidopsis thaliana					
23	L	S	D	D	V	R	S	R	S	N	L	G	W	V	D	V	Q	I	A	A	F	E	K	S	L	E	D	F	K	Q	-	-	c.elegans kinase					
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)					
16	I	D	-	-	-	-	V	Y	A	Y	A	F	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)					
27	Y	E	A	A	G	D	E	E	L	T	L	R	R	G	D	-	R	V	Q	V	L	S	Q	D	-	-	-	-	-	-	-	-	C	H.sapiens (Z48615)				
27	Y	E	A	A	G	D	E	E	L	T	L	R	R	G	D	-	R	V	Q	V	L	S	Q	D	-	-	-	-	-	-	-	-	C	Homo sapiens (Z48615)				
16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	F	K	D	A	V	F	D	G	S	-	-	-	-	-	-	Human raf1(W13107)					
16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	F	K	D	A	V	F	D	G	S	-	-	-	-	-	-	Human Raf1kinase(R98215)					
22	L	D	-	-	-	-	P	A	R	L	G	S	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)					
- - - - -																												Majority										
70														80														90										
48	I	F	G	S	D	E	A	F	S	K	V	N	L	N	Y	R	T	E	N	G	L	S	L	L	H	L	C	C	I	C	-	-	CARP2/prot					
8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2					
12	-	-	-	-	-	-	-	-	R	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3					
39	I	A	Q	R	K	L	G	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Arabidopsis thaliana					
53	H	M	C	P	E	N	A	-	-	-	-	-	-	-	-	-	E	L	K	S	T	Q	L	L	S	L	F	H	I	I	C	A	-	c.elegans kinase				
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)					
28	A	L	T	S	H	L	P	F	R	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)					
51	A	V	S	G	D	E	G	W	W	T	G	Q	L	-	-	-	P	S	G	R	V	G	V	F	P	S	N	Y	V	A	-	-	H.sapiens (Z48615)					
51	A	V	S	G	D	E	G	W	W	T	G	Q	L	-	-	-	P	S	G	R	V	G	V	F	P	S	N	Y	V	A	-	-	Homo sapiens (Z48615)					
26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human raf1(W13107)					
26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)					
34	V	Q	S	E	Q	K	S	R	P	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)					

Fig. 3A

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- - S - A - - - L Q - - L P N L R P - - - - L - E - - -																											Majority				
100									110									120													
78	G	G	K	K	S	H	I	R	T	L	-	-	M	L	K	G	L	R	P	-	-	-	-	-	S	R	L	T	CARP2/prot		
8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2		
14	-	-	S	L	R	S	K	L	P	L	E	P	S	L	P	N	L	P	C	N	P	S	S	S	K	T	N	R	-	A.thaliana3	
47	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Arabidopsis thaliana		
76	G	H	S	D	S	Q	P	E	K	L	Q	F	L	I	D	N	L	P	K	E	S	S	I	T	L	I	S	S	Q	S	c.elegans kinase
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)	
38	-	-	F	N	D	I	S	V	A	A	K	V	A	Y	E	N	L	R	P	K	I	P	T	S	-	C	P	L	-	D.Discoideum (U01064)	
78	P	G	A	P	A	A	P	A	G	L	Q	-	-	L	P	Q	E	I	P	F	H	E	L	Q	L	E	E	I	I	G	H.sapiens (Z48615)
78	P	G	A	P	A	A	P	A	G	L	Q	-	-	L	P	Q	E	I	P	F	H	E	L	Q	L	E	E	I	I	G	Homo sapiens (Z48615)
30	P	T	I	V	Q	-	-	-	-	Q	F	G	Y	Q	R	-	R	A	S	D	D	G	K	L	T	D	P	S	K	Human raf1(W13107)	
30	P	T	I	V	Q	-	-	-	-	Q	F	G	Y	Q	R	-	R	A	S	D	D	G	K	L	T	D	P	S	K	Human Raf1kinase(R98215)	
44	-	-	S	K	A	Q	R	H	P	M	T	Y	K	Q	R	S	L	S	P	L	P	E	T	Y	L	S	E	A	-	Soybean kinase(M67449)	
- - - - - R G A R T L V K K R F A A - - D D S																											Majority				
130									140									150													
99	R	N	G	F	T	A	L	H	L	A	V	Y	K	D	N	A	E	L	I	T	S	L	L	H	S	G	-	A	D	I	CARP2/prot
8	-	-	-	-	-	-	-	-	-	-	-	-	D	G	N	N	T	T	K	E	K	I	F	-	-	-	-	-	-	-	A.thaliana kinase2
40	-	-	-	-	-	-	-	-	-	-	Y	A	E	A	E	T	M	E	K	K	R	F	D	S	-	-	M	E	S	-	A.thaliana3
47	-	-	-	-	G	Q	F	S	T	V	W	L	A	Y	D	T	L	T	S	T	Y	V	A	L	K	I	Q	K	S	Arabidopsis thaliana	
106	A	N	G	F	T	P	L	H	I	A	I	Y	R	G	D	V	A	I	L	K	A	L	I	A	T	K	L	V	D	L	c.elegans kinase
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)	
63	-	-	-	-	-	-	-	-	-	-	F	I	-	-	R	K	L	I	N	R	C	W	A	P	-	-	L	P	S	D.Discoideum (U01064)	
106	V	G	G	F	G	K	V	Y	R	A	L	W	R	G	E	E	V	A	V	K	-	-	-	A	A	R	L	D	P	E	H.sapiens (Z48615)
106	V	G	G	F	G	K	V	Y	R	A	L	W	R	G	E	E	V	A	V	K	-	-	-	A	A	R	L	D	P	E	Homo sapiens (Z48615)
54	T	S	N	T	I	R	V	F	L	P	-	-	N	K	Q	R	T	V	V	N	V	R	N	G	M	S	L	H	D	C	Human raf1(W13107)
54	T	S	N	T	I	R	V	F	L	P	-	-	N	K	Q	R	T	V	V	N	V	R	N	G	M	S	L	H	D	C	Human Raf1kinase(R98215)
70	-	-	-	-	-	-	-	-	-	-	F	R	E	A	R	-	L	E	Q	K	R	F	S	T	-	-	P	N	P	Soybean kinase(M67449)	
- - - - - L - - L - - - - - G - - - - - G																											Majority				
160									170									180													
128	Q	Q	V	G	Y	G	G	L	T	A	L	H	I	A	T	I	A	G	H	L	E	A	A	D	V	L	L	Q	H	G	CARP2/prot
19	-	R	A	D	K	I	D	L	K	S	L	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2
57	W	-	-	-	-	-	S	M	I	L	E	S	E	N	V	E	T	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3
72	A	Q	Q	F	A	Q	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Arabidopsis thaliana
136	D	Q	S	G	R	H	L	L	P	A	L	H	L	A	A	M	I	G	D	S	E	M	L	T	I	L	L	N	S	G	c.elegans kinase
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)
78	D	R	P	T	F	N	D	I	L	K	L	-	F	D	H	L	E	G	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)
133	K	D	P	A	V	T	A	E	Q	V	C	Q	E	A	R	L	F	G	A	L	Q	H	P	N	I	I	A	L	R	G	H.sapiens (Z48615)
133	K	D	P	A	V	T	A	E	Q	V	C	Q	E	A	R	L	F	G	A	L	Q	H	P	N	I	I	A	L	R	G	Homo sapiens (Z48615)
82	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human raf1(W13107)
82	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)
86	R	R	E	K	R	I	M	G	K	L	L	N	K	D	S	R	E	T	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)

Fig. 3B

----- R -----																										Majority							
190										200										210													
158	A	N	V	N	I	Q	D	A	V	F	F	T	P	L	H	I	A	A	Y	Y	G	H	E	Q	V	T	R	L	L	L	CARP2/prot		
30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2		
69	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3		
80	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	H	E	I	E	F	L	S	A	A	A	D	G	D	L	-	Arabidopsis thaliana		
166	A	N	I	H	V	T	D	F	V	H	F	T	A	L	H	C	A	T	Y	F	G	Q	E	N	A	V	R	T	L	I	c.elegans kinase		
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)		
95	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)		
163	A	C	L	N	P	P	H	L	C	L	-	-	-	-	V	M	E	Y	A	R	G	G	A	L	S	R	V	L	A	H.sapiens (Z48615)			
163	A	C	L	N	P	P	H	L	C	L	-	-	-	-	V	M	E	Y	A	R	G	G	A	L	S	R	V	L	A	Homo sapiens (Z48615)			
91	-	-	L	Q	P	E	C	C	A	V	F	R	L	L	H	E	-	-	-	H	K	G	K	K	A	R	L	D	W	Human raf1(W13107)			
91	-	-	L	Q	P	E	C	C	A	V	F	R	L	L	H	E	-	-	-	H	K	G	K	K	A	R	L	D	W	Human Raf1kinase(R98215)			
104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)		
----- L -----																										Majority							
220										230										240													
188	K	F	G	A	D	V	N	V	S	G	E	V	G	D	R	P	L	H	L	A	S	A	K	G	F	L	N	I	A	K	CARP2/prot		
30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2		
69	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3		
95	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D	K	T	K	C	V	V	R	L	I	D	H	F	K	H	S	Arabidopsis thaliana		
196	S	A	S	A	N	L	N	L	G	G	A	V	N	D	R	P	I	H	L	A	A	A	K	G	L	T	S	I	T	K	c.elegans kinase		
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)		
95	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)		
188	G	R	R	V	P	P	H	V	-	-	-	L	V	N	W	A	V	Q	V	A	R	G	M	N	Y	L	H	N	D	A	H.sapiens (Z48615)		
188	G	R	R	V	P	P	H	V	-	-	-	L	V	N	W	A	V	Q	V	A	R	G	M	N	Y	L	H	N	D	A	Homo sapiens (Z48615)		
115	N	T	D	A	A	S	L	I	G	E	E	L	-	-	-	-	-	-	-	Q	V	D	F	L	D	H	-	-	-	-	Human raf1(W13107)		
115	N	T	D	A	A	S	L	I	G	E	E	L	-	-	-	-	-	-	-	Q	V	D	F	L	D	H	-	-	-	-	Human Raf1kinase(R98215)		
104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)		
----- L ----- L ----- K L A -----																										Majority							
250										260										270													
218	-	-	-	L	L	M	E	E	G	S	K	A	D	V	N	A	Q	D	N	E	D	H	V	P	L	H	F	C	S	R	CARP2/prot		
30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	Q	L	E	K	H	L	S	-	-	-	-	A.thaliana kinase2		
69	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3		
112	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	G	Q	H	L	C	-	Arabidopsis thaliana		
226	-	-	-	L	L	L	E	-	-	A	K	A	D	P	L	L	A	D	D	E	G	N	Q	A	L	H	Y	A	A	K	c.elegans kinase		
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)		
96	-	-	-	L	F	F	S	S	P	G	I	L	R	S	L	N	N	D	Q	E	V	E	R	E	L	Q	-	-	-	-	D.Discoideum (U01064)		
215	P	V	P	I	I	H	R	D	L	K	S	I	N	I	L	I	L	E	A	I	E	N	H	N	L	A	-	-	-	-	H.sapiens (Z48615)		
215	P	V	P	I	I	H	R	D	L	K	S	I	N	I	L	I	L	E	A	I	E	N	H	N	L	A	-	-	-	-	Homo sapiens (Z48615)		
134	-	V	P	L	T	T	H	N	F	A	R	K	T	F	L	-	-	-	-	-	-	-	-	-	K	L	A	F	C	D	-	Human raf1(W13107)	
134	-	V	P	L	T	T	H	N	F	A	R	K	T	F	L	-	-	-	-	-	-	-	-	-	-	K	L	A	F	C	D	-	Human Raf1kinase(R98215)
105	-	-	-	-	-	-	E	S	S	S	K	S	P	S	R	S	P	N	R	O	V	K	S	K	N	R	-	-	-	-	Soybean kinase(M67449)		

Fig. 3C

- - - - - F L - - - - - Y - - -																									Majority										
280 290 300																																			
245	F	G	H	H	D	I	V	K	Y	L	L	Q	S	D	L	E	V	Q	P	H	V	V	-	-	N	I	Y	G	-	-	CARP2/prot				
38	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2				
69	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3				
119	-	-	-	-	M	V	L	E	F	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Arabidopsis thaliana				
251	S	G	S	L	V	I	L	N	M	L	I	K	Q	V	R	G	T	N	D	R	I	C	A	R	N	L	Y	G	-	-	c.elegans kinase				
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)				
119	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)				
241	D	T	V	L	K	I	T	D	F	G	L	A	R	E	W	H	K	T	T	K	M	S	A	A	G	T	Y	A	W	M	H.sapiens (Z48615)				
241	D	T	V	L	K	I	T	D	F	G	L	A	R	E	W	H	K	T	T	K	M	S	A	A	G	T	Y	A	W	M	Homo sapiens (Z48615)				
154	-	-	-	-	I	C	Q	K	F	L	L	N	G	F	R	-	-	-	-	-	-	-	-	-	-	C	Q	T	C	G	Y	K	F	H	Human raf1(W13107)
154	-	-	-	-	I	C	Q	K	F	L	L	N	G	F	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)		
125	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)		
- - - - - L - - - - - K - - VWS - I L Q - L L - - - -																									Majority										
310 320 330																																			
271	-	D	T	P	L	H	L	A	C	Y	N	G	K	F	E	V	A	K	E	I	I	Q	I	S	G	T	E	S	L	T	CARP2/prot				
38	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	V	W	S	R	N	L	E	-	-	-	-	-	V	N	A.thaliana kinase2		
69	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3			
125	G	D	S	L	L	R	L	I	R	Y	N	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Arabidopsis thaliana		
279	-	D	T	A	L	H	L	S	C	Y	S	G	R	L	D	I	V	K	S	I	L	D	S	S	P	T	N	I	V	N	c.elegans kinase				
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)			
119	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)			
271	A	P	E	V	I	R	L	S	L	F	S	K	S	S	D	V	W	S	-	-	F	G	V	L	L	W	E	L	L	T	H.sapiens (Z48615)				
271	A	P	E	V	I	R	L	S	L	F	S	K	S	S	D	V	W	S	-	-	F	G	V	L	L	W	E	L	L	T	Homo sapiens (Z48615)				
174	E	H	C	S	T	K	V	P	-	-	-	T	M	C	V	D	W	S	N	I	R	Q	L	L	L	-	-	-	-	-	-	-	Human raf1(W13107)		
174	E	H	C	S	T	K	V	P	-	-	-	T	M	C	V	D	W	S	N	I	R	Q	L	L	L	-	-	-	-	-	-	-	Human Raf1kinase(R98215)		
125	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)		
- E - - - - -																									Majority										
340 350 360																																			
300	K	E	N	I	F	S	E	T	A	F	H	S	A	C	T	Y	G	K	S	I	D	L	V	K	F	L	L	D	Q	N	CARP2/prot				
48	P	K	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2			
73	K	G	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3			
137	-	-	-	-	Y	K	G	L	K	L	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Arabidopsis thaliana		
308	M	E	N	V	F	S	E	T	P	L	H	A	A	C	T	G	G	K	S	I	E	L	V	S	F	L	M	K	Y	P	c.elegans kinase				
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)			
135	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)			
299	G	E	V	P	Y	R	E	I	D	-	A	L	A	V	A	Y	G	-	-	V	A	M	N	K	L	T	L	P	I	P	H.sapiens (Z48615)				
299	G	E	V	P	Y	R	E	I	D	-	A	L	A	V	A	Y	G	-	-	V	A	M	N	K	L	T	L	P	I	P	Homo sapiens (Z48615)				
196	-	-	-	-	F	P	N	S	T	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human raf1(W13107)		
196	-	-	-	-	F	P	N	S	T	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)		
143	V	E	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)		

Fig. 3D

	430	440	450	Majority
371	- - - - -	C D P S R S S G E K - - - - -	- - - - -	CARP2/prot
54	- - - - -	- - - - -	- - - - -	A.thaliana kinase2
79	- - - - -	- - - - -	- - - - -	A.thaliana3
162	E L G M I H - - - - -	- - - - - S D L K P E N I L L C S T I D	- - - - -	Arabidopsis thaliana
390	- - - - -	- A G P G T N R P S K V A S A I M A L N R S D T	- - - - -	c.elegans kinase
6	- - - - -	- - - - -	- - - - -	D.discoideum (A35670)
135	- - - - -	- - - - -	- - - - -	D.Discoideum (U01064)
381	K L E I Q H M F D D L R T K E K E L R S R E E E L L R A - -	- - - - -	- - - - -	H.sapiens (Z48615)
381	K L E I Q H M F D D L R T K E K E L R S R E E E L L R A - -	- - - - -	- - - - -	Homo sapiens (Z48615)
248	E - - - - -	- G S L S Q R Q R S T S T P N V H M V S T T L	- - - - -	Human raf1(W13107)
248	E - - - - -	- G S L S Q R Q R S T S T P N V H M V S T T L	- - - - -	Human Raf1kinase(R98215)
149	- - - - -	- - - - -	- - - - -	Soybean kinase(M67449)

Fig. 3E

9/35

----- W E L D -----										Majority
460			470			480				
381	-----	DEQ	TCL	MW	AYE	KGH	DA			CARP2/prot
54	-----	-----	-----	WE	ID	-----	-----			A.thaliana kinase2
79	-----	-----	-----	WT	AD	-----	-----			A.thaliana3
183	PAKDP	-----	-----	-----	-----	VR	SG			Arabidopsis thaliana
413	PSSNASYNSTVSLDDQQTPVIWAYERGHDA									c.elegans kinase
6	-----	-----	-----	WE	TQ	SS	-----			D.discoideum (A35670)
135	-----	-----	-----	EI	K	-----	-----			D.Discoideum (U01064)
409	AQEQR	FQEEQLRRREQE	LAEREMDIVERE							H.sapiens (Z48615)
409	AQEQR	FQEEQLRRREQE	LAEREMDIVERE							Homo sapiens (Z48615)
271	PVDS	RMIEDAIRSHSESASPSALSSSPNN								Human raf1(W13107)
271	PVDS	RMIEDAIRSHSESASPSALSSSPNN								Human Raf1kinase(R98215)
149	-----	-----	-----	WN	VD	-----	-----			Soybean kinase(M67449)
L -----										Majority
490			500			510				
397	IVTLLKHYK	-----	RPQ	DEL	PCNEY	SQPG	-----			CARP2/prot
58	-----	-----	-----	-----	-----	-----	-----			A.thaliana kinase2
83	-----	-----	-----	-----	-----	-----	-----			A.thaliana3
192	LTPLL	-----	EK	PEGNANGGA	-----	STMNLI				Arabidopsis thaliana
443	IVALLKHYAA	RTVEGDVCSEYS	-----	S	-----	-----	-----			c.elegans kinase
12	-----	LSHPPS	-----	-----	-----	-----	-----			D.discoideum (A35670)
138	-----	-----	-----	-----	-----	-----	-----			D.Discoideum (U01064)
438	LHLLMCQLS	QEKPRVRKRKGNFKRAVLKLR								H.sapiens (Z48615)
438	LHLLMCQLS	QEKPRVRKRKGNFKRAVLKLR								Homo sapiens (Z48615)
300	LSP	-----	-----	-----	TGWS	QPK	-----			Human raf1(W13107)
300	LSP	-----	-----	-----	TGWS	QPK	-----			Human Raf1kinase(R98215)
153	-----	-----	-----	-----	-----	-----	-----			Soybean kinase(M67449)
----- P ----- L ----- R -----										Majority
520			530			540				
421	GDGSYVSVSP	PLGKIKSMTKEKADILLRA								CARP2/prot
58	-----	-----	-----	-----	-----	-----	-----			A.thaliana kinase2
83	-----	-----	-----	-----	-----	-----	-----			A.thaliana3
214	E	-----	-----	-----	-----	KKL	KRRA			Arabidopsis thaliana
466	GESSYTPLPSP	MGRLTSLTRDKADLLQLRS								c.elegans kinase
21	-----	PPPPPPPPQLP	-----	-----	-----	-----	-----			D.discoideum (A35670)
138	-----	-----	-----	-----	-----	-----	-----			D.Discoideum (U01064)
468	EGSSHISLPS	SGFEH	-----	KITVQASPTLDKRRK						H.sapiens (Z48615)
468	EGSSHISLPS	SGFEH	-----	KITVQASPTLDKRRK						Homo sapiens (Z48615)
310	-----	TPVPAQRERAPVSGTQEKNKIRPRG								Human raf1(W13107)
310	-----	TPVPAQRERAPVSGTQEKNKIRPRG								Human Raf1kinase(R98215)
153	-----	-----	-----	-----	-----	-----	-----			Soybean kinase(M67449)

Fig. 3F

-- D - - - - - L S E L E F G L R I G S G S F G T V Y		Majority
550	560	570
451 GLPSHF - - HLQLSEIEFHEIIGSGSGSFGKVY		CARP2/prot
58 - - - - - LAKLETSNVIARGTYGTVY		A.thaliana kinase2
83 - - - - - LSQLFIGNKFASGAHSRIY		A.thaliana3
222 KRA - - - - -		Arabidopsis thaliana
496 ALPAPF - - HLC LAEIEFQESIGSGSGSFGKVY		c.elegans kinase
81 - VRSEY - - EIDFNELEFQGQTIGKGFGEVK		D.discoideum (A35670)
138 - - - - - FDEVAIVEKVGAGSFANVF		D.Discoideum (U01064)
496 GSDGAS - - PPASPSIIPRLRAIRLTPVDCG		H.sapiens (Z48615)
496 GSDGAS - - PPASPSIIPRLRAIRLTPVDCG		Homo sapiens (Z48615)
335 QRDSSYYWEIEASEVMLSTRIGSGSGSFGTVY		Human raf1(W13107)
335 QRDSSYYWEIEASEVMLSTRIGSGSGSFGTVY		Human Raf1kinase(R98215)
153 - - - - - MSQLFFGLKFAHGAHSRLY		Soybean kinase(M67449)
KGIYRG - DVAVKILKRGDP - - E - - - - K - E		Majority
580	590	600
479 KGRCRNKIVAIKR - YRAN - - - - TYCSKSD		CARP2/prot
77 KGIYDGDQDVAVKVLDWEDDGNETTAKTATN		A.thaliana kinase2
102 RGIYKQRAVAVKMRIPTHKEETR - - AKLE		A.thaliana3
225 - - - - -		Arabidopsis thaliana
524 KGTYRGKLVAVKR - YRAM - - - - AFGCKSE		c.elegans kinase
58 RGYWRETDVAIKIIRYRDQ - - - - FKTKSS		D.discoideum (A35670)
157 LGIWNGYKVAIKILKNESISNDEK - - - -		D.Discoideum (U01064)
524 GSSSGSSSSGSGGTWSRGGPPKKEELVGGKK		H.sapiens (Z48615)
524 GSSSGSSSSGSGGTWSRGGPPKKEELVGGKK		Homo sapiens (Z48615)
365 KGKWHG - DVAVKILKVVDPTPE - - - - - Q		Human raf1(W13107)
365 KGKWHG - DVAVKILKVVDPTPE - - - - - Q		Human Raf1kinase(R98215)
172 HGVYKDEAVAVKIIMVPEDDGNALASRLE		Soybean kinase(M67449)
KQ - FRNEVSVLSKLRHPNVVQFVGA - L - -		Majority
610	620	630
503 VDMFCREVSILCQLNHPCVVIQFVGACL - N -		CARP2/prot
107 RALFRQEVTVVWHKLNHPNVTKFVGASMGTT		A.thaliana kinase2
130 QQ - FKSEVALLSRLFHPNIVQFIAACK - - -		A.thaliana3
225 - - - - - VAKISERRVSMVTGE - - - -		Arabidopsis thaliana
548 TDMLCREVSILSRLAHPNVVAFVGTSL - D -		c.elegans kinase
82 LVMFQNEVGILSKLRHPNVVQFLGACTAG -		D.discoideum (A35670)
181 - - - FIKEVSSSLIKSHHPNVVTFMGA - - - -		D.Discoideum (U01064)
554 KGRTWGPSSTLQKERVGGGEERLKG - - LGEG		H.sapiens (Z48615)
554 KGRTWGPSSTLQKERVGGGEERLKG - - LGEG		Homo sapiens (Z48615)
387 FQAFRNEVAVLRKTRHVNILLFMGY - - - -		Human raf1(W13107)
387 FQAFRNEVAVLRKTRHVNILLFMGY - - - -		Human Raf1kinase(R98215)
202;KQ - FIREVTLLSRLHHQNVIKFSAACR - - -		Soybean kinase(M67449)

Fig. 3G

```

- - - - - D P D H L C I V T E Y L S G G S L Majority
          640          650          660
531 - - - - - D P S Q F A I V T Q Y I S G G S L CARP2/prot
137 N L N I R S A D S K G S L P Q Q A C C V V V E Y L P G G T L A.thaliana kinase2
156 - - - - - K P P V Y C I I T E Y M S Q G N L A.thaliana3
240 - - - - - Arabidopsis thaliana
576 - - - - - D P S Q F A I I T E F V E N G S L c.elegans kinase
111 - - - - - G E D H H C I V T E W M G G G S L D.discoideum (A35670)
203 - - - - - R I D P P - - C I F T E Y L Q G G S L D.Discoideum (U01064)
582 S K Q W S S S A P N L G K S P K H T P I A P G F A S L N E M H.sapiens (Z48615)
582 S K Q W S S S A P N L G K S P K H T P I A P G F A S L N E M Homo sapiens (Z48615)
412 - - - - - M T K D N L A I V T Q W C E G S S L Human raf1(W13107)
412 - - - - - M T K D N L A I V T Q W C E G S S L Human Raf1kinase(R98215)
228 - - - - - K P P V Y C I I T E Y L A E G S L Soybean kinase(M67449)

R E H L H - E D - K F S L L P - - - - - L K I A L D I Majority
          670          680          690
548 F S L L H E Q K - - - R I L D - - L Q S K - - L I I A V D V CARP2/prot
167 K Q H L I - R H K S K K L A F K A V - - - - I K L A L D L A.thaliana kinase2
173 R M Y L N - K K E P Y S L S I E T V - - - - L R L A L D I A.thaliana3
240 - - - - - Arabidopsis thaliana
593 F R R E N G E R K N Y R V M D - - P A F R - - L R I S L D V c.elegans kinase
128 R Q F L T D H - - - F N L L E Q N P H I R - - L K L A L D I D.discoideum (A35670)
220 Y D V L H - - I Q K I K L N P L M M - - - - Y K M I H D L D.Discoideum (U01064)
612 E E F A E A E D G G S S V P P S P Y S T P S Y L S V P L P A H.sapiens (Z48615)
612 E E F A E A E D G G S S V P P S P Y S T P S Y L S V P L P A Homo sapiens (Z48615)
430 Y K H L H V Q E T K F Q M F Q - - - - - L I D I A R Q T Human raf1(W13107)
430 Y K H L H V Q E T K F Q M F Q - - - - - L I D I A R Q T Human Raf1kinase(R98215)
245 R A Y L H - K L E H Q T I S L Q K L - - - - I A F A L D I Soybean kinase(M67449)

A R G M E Y L H - - - A Q P I I H R D L K S H N I L L D E - Majority
          700          710          720
571 A K G M E Y L H N - L T Q P I I H R D L N S H N I L L Y - - CARP2/prot
191 A R G L S Y L H - - - S E K I V H R D V K T E N M L L D A Q A.thaliana kinase2
197 S R G M E Y L H - - - S Q G V I H R D L K S N N L L L N D E A.thaliana3
240 - - - - - E A S S K T E K S L D G I D M - - - - Arabidopsis thaliana
619 A R G M R Y L H E S A A K P V I H R D L N S H N I L I H - - c.elegans kinase
153 A K G M N Y L H G W - T P P I L H R D L S S R N I L L D H N D.discoideum (A35670)
243 S L G M E H L H - - - S I Q M L H R D L T S K N I L L D E F D.Discoideum (U01064)
642 E P S P G A R A P W E P T P S A P P A R W G H G - - - - A R H.sapiens (Z48615)
642 E P S P G A R A P W E P T P S A P P A R W G H G - - - - A R Homo sapiens (Z48615)
453 A Q G M D Y L H - - - A K N I I H R D M K S N N I F L H E G Human raf1(W13107)
453 A Q G M D Y L H - - - A K N I I H R D M K S N N I F L H E G Human Raf1kinase(R98215)
269 A R G M E Y I H - - - S Q G V I H R D L K P E N I L I N E D Soybean kinase(M67449)

```

Fig. 3H

12/35

- R V K - - - - - I A D F G L A R - L E A - Majority		
730	740	750
598 - - - - - E D G H A V V A D F G E S R F L Q S -		CARP2/prot
218 K N L K - - - - - I A D F G V A R - V E A -		A.thaliana kinase2
224 M R V K - - - - - V A D F G T S C - L E T -		A.thaliana3
255 - - - - - R C K V V D F G N A C - - - - W		Arabidopsis thaliana
647 - - - - - A D G R S V V A D F G E S R F V C Q -		c.elegans kinase
182 I D P K N P L V S S R Q D I K C K I S D F G L S R - L K K -		D.discoideum (A35670)
270 K N I K - - - - - I A D F G L A - - - T T -		D.Discoideum (U01064)
668 R R C D L A L L G C - - - - - A T L L G A V G L G A D -		H.sapiens (Z48615)
668 R R C D L A L L G C - - - - - A T L L G A V G L G A D -		Homo sapiens (Z48615)
480 L T V K - - - - - I G D F G L A T V K S R W		Human raf1(W13107)
480 L T V K - - - - - I G D F G L A T V K S R W		Human Raf1kinase(R98215)
296 N H L K - - - - - I A D F G I A C - E E A -		Soybean kinase(M67449)
L A D D Q A A D G T G T L R W M A P E V F I - - K G G P Y S Majority		
760	770	780
616 L D E D N M T K Q P G N L R W M A P E V F T - - Q C T R Y T		CARP2/prot
233 L N P K D M T G R T G T L G Y M A P E V - I - - D G K P Y N		A.thaliana kinase2
239 - Q C R E A K G N M G T Y R W M A P E M - I - - K E K P Y T		A.thaliana3
267 - A D K Q F A E E I Q T R Q Y R A P E V I L K - - - S G Y S		Arabidopsis thaliana
665 R E D E N L T K Q P G N L R W M A P E V F S - - Q S G K Y D		c.elegans kinase
210 E Q A S Q M T Q S V G C I P Y M A P E V F - - - K G D S N S		D.discoideum (A35670)
283 L S D D M T L S G I T N P R W R S P E L - T - - K G L V Y N		D.Discoideum (U01064)
690 V A E A R A A D G E E Q R R W L D G L F F P - - R A G R F P		H.sapiens (Z48615)
690 V A E A R A A D G E E Q R R W L D G L F F P - - R A G R F P		Homo sapiens (Z48615)
497 S G S Q Q V E Q P T G S V L W M A P E V I R M Q D N N P F S		Human raf1(W13107)
497 S G S Q Q V E Q P T G S V L W M A P E V I R M Q D N N P F S		Human Raf1kinase(R98215)
311 - S C D L L A D D P G T Y R W M A P E M - I - - K R K S Y G		Soybean kinase(M67449)
R K V D V Y S F G L V L W E L V T G E L P F A H L N P - V Q Majority		
790	800	810
644 I K A D V F S Y A L C L W E I L T G E I P F A H L K P - A A		CARP2/prot
260 R R C D V Y S F G I C L W E I Y C C D M P Y P D L S F - V D		A.thaliana kinase2
265 R K V D V Y S F G I V L W E L T T A L L P F Q G M T P - V Q		A.thaliana3
293 F S V D M W S F G C T A F E L V T G D M L F A P K D G N - -		Arabidopsis thaliana
693 R K V D V F S F A L V I W E I H T A E L P F S H L K P - A A		c.elegans kinase
237 E K S D V Y S Y G M V L F E L L T S D E P Q Q D M K P - M K		D.discoideum (A35670)
310 E K V D V Y S F G L V V Y E I Y T G K I P F E G L D G - T A		D.Discoideum (U01064)
718 R G L S P P A R P H G R R E D V G P G L G L A P S A T L V S		H.sapiens (Z48615)
718 R G L S P P A R P H G R R E D V G P G L G L A P S A T L V S		Homo sapiens (Z48615)
527 F Q S D V Y S Y G I V L Y E L M T G E L P Y S H I N N R D Q		Human raf1(W13107)
527 F Q S D V Y S Y G I V L Y E L M T G E L P Y S H I N N R D Q		Human Raf1kinase(R98215)
337 K K V D V Y S F G L I L W E M L T G T I P Y E D M N P - I Q		Soybean kinase(M67449)

Fig. 31

A A F A V A Y G N A R P P L P S D C - - - - P A A L S S L I Majority															
820					830					840					
673	A A A D M A Y H H I R P P I G Y S - - - - I P K P I S S L L										CARP2/prot				
289	V S S A V V L H N L R P E I P R C C - - - - P T A L A G I M										A.thaliana kinase2				
294	A A F A V A E K N E R P P L P A S C - - - - Q P A L A H L I										A.thaliana3				
321	- - - - - G Y G E D E D H L A - - - - - - - - - - -										Arabidopsis thaliana				
722	A A A E M T Y K R G R P T L P N Q P T A Q F P A H I L S L I										c.elegans kinase				
266	M A H L A A Y E S Y R P P I P L T T S S K W K E - - - - I L										D.discoideum (A35670)				
339	S A A K A A F E N Y R P A I P P D C - - - - P V S L R K L I										D.Discoideum (U01064)				
748	L S S V S D C N S T R S L L R S D S D E A A P A A P S P P P										H.sapiens (Z48615)				
748	L S S V S D C N S T R S L L R S D S D E A A P A A P S P P P										Homo sapiens (Z48615)				
557	I I F M V G R G Y A S P D L S K L Y K N C - P K A M K R L V										Human raf1(W13107)				
557	I I F M V G R G Y A S P D L S K L Y K N C - P K A M K R L V										Human Raf1kinase(R98215)				
366	A A F A V V N K N S R P I I P S N C - - - - P P A M R A L I										Soybean kinase(M67449)				
A Q C W A P N P S K R P S F S E I V - - - - L E - - - - - Majority															
850					860					870					
699	I R G W N A C P E G R P E F S E V V M K - L E E C L C N I E										CARP2/prot				
315	K T C W D G N P Q K R P E M K E V V K M - L E G V - - D T S										A.thaliana kinase2				
320	K R C W S E N P S K R P D F S N I V A V - L E K Y - - D E C										A.thaliana3				
331	- - - - - - - - - - - - - - - - L M M E L - - - - -										Arabidopsis thaliana				
752	P Q A W H P E S S R R P D F V E I V - - - - - - - - - A										c.elegans kinase				
292	T Q C W D S N P D S R P T F K Q I I V H - L K E - - - - -										D.discoideum (A35670)				
365	T K C W A S D P S Q R P S F T E I L T E - L E T M - - K S K										D.Discoideum (U01064)				
778	S P P - A P T P T P S P S T N P L V D L E L E S F K K D P R										H.sapiens (Z48615)				
778	S P P - A P T P T P S P S T N P L V D L E L E S F K K D P R										Homo sapiens (Z48615)				
586	A D C V K K V K E E R P L F P Q I L - - - - - - - - -										Human raf1(W13107)				
586	A D C V K K V K E E R P L F P Q I L - - - - - - - - -										Human Raf1kinase(R98215)				
392	E Q C W S L Q P D K R P E F W Q V V K I - L E Q F - - E S -										Soybean kinase(M67449)				
- - - - P - S V T S - - S L S L - - - - T P S - - - - - Majority															
880					890					900					
728	L - M S P A S S N S S G S L S P - - - - S S S S D C L V N R										CARP2/prot				
342	K - G G G M I P E - - - - - - - - - - - - - - -										A.thaliana kinase2				
347	V - K E G L P L T S H A S L T K - - - - T K K A - - - - -										A.thaliana3				
336	- - - - - - - - - - - - - - - - L G K M P R K I A I G G A - - - -										Arabidopsis thaliana				
771	L - L E P H V E S T H T D I S A - - - - P S T V - - - - -										c.elegans kinase				
315	- - M E D Q G V S S F A S V P V - - - - Q T - - - - -										D.discoideum (A35670)				
392	F - I K Q L S F L N D - - L I Q - - - - N P D - - - - -										D.Discoideum (U01064)				
807	Q S L T P T H V T A A C A V S R G H R R T P S D G A L G Q R										H.sapiens (Z48615)				
807	Q S L T P T H V T A A C A V S R G H R R T P S D G A L G Q R										Homo sapiens (Z48615)				
604	- - - - - - - - - - - S S I E L L Q H S L P K - - - - I N R										Human raf1(W13107)				
604	- - - - - - - - - - - S S I E L L Q H S L P K - - - - I N R										Human Raf1kinase(R98215)				
418	- - - - - - S L A S D G T L S L - - - - V P N P - - - - -										Soybean kinase(M67449)				

Fig. 3J

----- H -----										Majority																						
910					920					930																						
753	G	G	P	G	R	S	-	H	V	A	A	L	R	S	R	F	E	L	E	Y	A	L	N	A	R	S	Y	A	A	L	CARP2/prot	
350	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2
366	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3
349	-	-	-	-	K	S	K	D	Y	F	D	R	H	G	D	L	K	R	I	R	R	L	-	-	-	-	K	Y	W	P	L	Arabidopsis thaliana
790	-	-	-	-	-	S	-	Q	L	T	S	Q	W	E	Q	L	S	V	A	-	P	P	P	A	S	K	F	P	P	I	c.elegans kinase	
331	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)
408	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)
837	G	P	P	E	P	A	G	H	G	P	G	P	R	D	L	L	D	F	P	R	L	P	D	P	Q	A	L	F	P	A	H.sapiens (Z48615)	
837	G	P	P	E	P	A	G	H	G	P	G	P	R	D	L	L	D	F	P	R	L	P	D	P	Q	A	L	F	P	A	Homo sapiens (Z48615)	
619	S	A	S	E	P	S	L	H	R	A	A	H	T	E	D	I	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human raf1(W13107)
619	S	A	S	E	P	S	L	H	R	A	A	H	T	E	D	I	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)
432	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)
----- L T - D P - K G P ----- D																														Majority		
940										950										960												
782	S	Q	S	A	G	Q	Y	S	S	-	-	Q	G	L	S	L	E	E	M	K	R	S	L	Q	Y	T	P	-	I	D	CARP2/prot	
350	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D	Q	S	R	G	C	F	C	-	-	-	-	-	-	A.thaliana kinase2
366	-	-	-	-	-	-	-	-	-	-	-	-	-	I	L	D	H	L	K	G	C	V	T	S	I	S	-	-	S	-	-	A.thaliana3
372	D	R	-	-	-	-	-	-	-	-	-	-	L	L	I	D	K	Y	K	L	P	E	A	E	A	K	E	F	A	-	-	Arabidopsis thaliana
813	L	S	A	L	H	G	I	A	A	-	-	T	G	-	T	V	E	E	L	R	Q	R	-	-	-	-	-	-	I	D	c.elegans kinase	
331	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)
408	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)
867	R	R	R	P	P	E	F	P	G	R	P	T	T	L	T	F	A	P	R	P	R	P	A	A	S	R	P	R	L	D	H.sapiens (Z48615)	
867	R	R	R	P	P	E	F	P	G	R	P	T	T	L	T	F	A	P	R	P	R	P	A	A	S	R	P	R	L	D	Homo sapiens (Z48615)	
636	-	-	-	-	-	-	-	-	-	-	-	-	-	A	C	T	L	T	T	S	P	-	-	-	-	-	-	-	-	-	-	Human raf1(W13107)
636	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	C	T	L	T	T	S	P	-	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)
432	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	W	D	H	K	K	G	L	L	H	W	I	Q	K	L	G	Soybean kinase(M67449)
P F ----- L - I - P ----- P -----																														Majority		
970										980										990												
809	K	Y	-	-	-	-	-	-	-	G	Y	V	S	D	P	M	S	S	M	H	F	H	S	C	R	N	S	S	S	F	CARP2/prot	
358	-	F	-	-	-	-	-	-	-	-	A	P	A	R	G	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana kinase2
380	P	F	-	-	-	-	-	-	-	-	S	S	S	S	V	P	V	N	-	-	-	-	-	-	-	-	-	-	-	-	-	A.thaliana3
391	E	F	-	-	-	-	L	T	P	I	L	E	F	A	P	E	K	R	P	T	A	Q	Q	C	-	-	-	-	-	L	Arabidopsis thaliana	
834	N	N	-	-	-	-	-	-	-	-	G	Y	V	I	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	c.elegans kinase
333	T	G	-	-	-	-	-	-	-	-	V	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.discoideum (A35670)
422	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D.Discoideum (U01064)
897	P	W	K	L	V	S	F	G	R	T	L	T	I	S	P	P	S	R	P	D	T	P	E	S	P	G	P	P	S	V	H.sapiens (Z48615)	
897	P	W	K	L	V	S	F	G	R	T	L	T	I	S	P	P	S	R	P	D	T	P	E	S	P	G	P	P	S	V	Homo sapiens (Z48615)	
644	-	-	R	L	P	V	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human raf1(W13107)
644	-	-	R	L	P	V	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human Raf1kinase(R98215)
448	P	L	-	-	-	-	-	-	-	-	H	Q	N	S	G	P	V	P	K	P	K	F	-	-	-	-	-	-	-	-	-	Soybean kinase(M67449)

Fig. 3K

		----- Majority	
		1000	1010
832	E - - - - - D S S		CARP2/prot
364			A.thaliana kinase2
390	- - - - - A		A.thaliana3
412	D H P W M N V T T Q N D A E N V D D Q M N N L H I K G		Arabidopsis thaliana
841	- - - - - K S		c.elegans kinase
337	- - - - - A		D.discoideum (A35670)
422			D.Discoideum (U01064)
927	Q P T L L D M D M E G Q N Q D S T V P L C G A H G S H		H.sapiens (Z48615)
927	Q P T L L D M D M E G Q N Q D S T V P L C G A H G S H		Homo sapiens (Z48615)
648			Human raf1(W13107)
648			Human Raf1kinase(R98215)
462	- - - - - T		Soybean kinase(M67449)

Fig. 3L

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam3.4/Pfam  
Sequence file: /tmp/orfanal.13255.aa

Query: sequence13252

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
ank	PF00023 Ank repeat	207.5	2e-58	9
pkinase	PF00069 Eukaryotic protein kinase domain	201.9	9.9e-57	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
ank	1/9	66	99	1	33	3.2	12
ank	2/9	100	132	1	33	34.0	3.4e-06
ank	3/9	133	165	1	33	44.5	2.4e-09
ank	4/9	168	198	1	33	34.6	2.3e-06
ank	5/9	199	233	1	33	28.1	0.00021
ank	6/9	234	268	1	33	15.4	0.28
ank	7/9	269	302	1	33	20.6	0.037
ank	8/9	306	338	1	33	3.3	11
ank	9/9	339	371	1	33	35.4	1.3e-06
pkinase	1/1	463	716	1	273	201.9	9.9e-57

Alignments of top-scoring domains:

ank: domain 1 of 9, from 66 to 99: score 3.2, E = 12

```

*->nGnTPLHLAaryg.nvevklLLehGAdvnartk<-*
nG++ LHL+++ g++ + ++ L+ +G + t+
sequence13 66 NGLSLLHLCCICGgKKSHIRTLMLKGLRPSRLTR 99

```

ank: domain 2 of 9, from 100 to 132: score 34.0, E = 3.4e-06

```

*->nGnTPLHLAarygnvevklLLehGAdvnartk<-*
nG+T+LHLA++++n e++ LL GAd+ + +
sequence13 100 NGFTALHLAVYKDNAELITSLHSGADIQQVGY 132

```

ank: domain 3 of 9, from 133 to 165: score 44.5, E = 2.4e-09

```

*->nGnTPLHLAarygnvevklLLehGAdvnartk<-*
G+T+LH+A ++g++e +++LL+hGA+vn+++
sequence13 133 GGLTALHIATIAGHLEAADVLLQHGANVNIQDA 165

```

ank: domain 4 of 9, from 168 to 198: score 34.6, E = 2.3e-06

```

*->nGnTPLHLAarygnvevklLLehGAdvnartk<-*
+TPLH+Aa+yg+ +v +lLL+ GAdvn+ +
sequence13 168 --FTPLHIAAAYGHEQVTRLLLKFGADVNVSGE 198

```

ank: domain 5 of 9, from 199 to 233: score 28.1, E = 0.00021

```

*->nGnTPLHLAarygnvevklLLe..hGAdvnartk<-*
G+ PLHLA+ +g +++klL+e++ Advna+++
sequence13 199 VGDRPLHLASAKGFLNIAKLLMEegSKADVNAQDN 233

```

Fig. 4A

ank: domain 6 of 9, from 234 to 268: score 15.4, E = 0.28  
\*->nGnTPLHLAarygnvevklLLe..hGAdvnartk<-\*  
+ PLH ++r g+ ++vk+LL+++ +++++  
sequence13 234 EDHVPLHFCSRFGHHDIVKYLLQsdLEVQPHVVNI 268

ank: domain 7 of 9, from 269 to 302: score 20.6, E = 0.037  
\*->nGnTPLHLAarygnvevklLLe.hGAdvnartk<-\*  
G+TPLHLA+++g+ ev+k ++ G+ + +  
sequence13 269 YGDTPLHLACYNGKFEVAKEIIQISGTESLTKEN 302

ank: domain 8 of 9, from 306 to 338: score 3.3, E = 11  
\*->nGnTPLHLAaryg.nvevklLLe.hGAdvnartk<-\*  
T+ H A+ yg+++++vk+LL+++ ++n + +  
sequence13 306 --ETAFHSACTYgKSIDLVKFLLDqNVININHQGR 338

ank: domain 9 of 9, from 339 to 371: score 35.4, E = 1.3e-06  
\*->nGnTPLHLAarygnvevklLLe.hGAdvnartk<-\*  
+G+T LH A+++g++++v++LL++GAd n +  
sequence13 339 DGHTGLHSACYHGHIRLVQFLLDNGADMNLVAC 371

pkinase: domain 1 of 1, from 463 to 716: score 201.9, E = 9.9e-57  
\*->yelleklGeGsfgKvYkakhktgkivAvKilk.....kesls..lr  
+e+++G+GsfgKvYk++ + +kivA+K + ++ +k++++ r  
sequence13 463 IEFHEIIGSGSFGKVYKGRCR-NKIVAIAKRYRantycsKSDVDmFCR 508

EiqilkrIsHpNIvrlIlgvfedtdhlylvmEymegGdLfdylrrng.pl  
E++il +l+Hp ++++ g++ ++++ + +v++y gG+Lf++l+++++ l  
sequence13 509 EVSILCQLNHPCViqFVGAVLNDPSQFAIVTQYISGGSFLSLLHEQKrIL 558

sekeakkialQilrGleYlHsng..ivHRDLKpeNILldengtviKiaDFG  
+ + + ia ++++G+eYLH+ ++i+HRDL + NILl e+g+ +aDFG  
sequence13 559 DLQSKLIIAVDVAKGMEYLHNLTqpIIHRDLNSHNILLYEDGHAVVADFG 608

LArll.....eklttfvGTpwYmmAPEvileg.rgysskvDvWSlGvily  
+r+l++ ++ +tt G +++m APEv + + y+ k+Dv S+ L+  
sequence13 609 ESRFLqsldeDNMTKQPGNLRWM-APEV-FTQcTRYTIKADVFSYALCLW 656

Elltgplfp gadlpaftggdevdqliifvklPfsdelpktridpleel  
E+ltg ++Pf + +p ++  
sequence13 657 EILTG-----EIPFAH-----LKPAAAA 674

frikkr..rlplpsncSeelkdLlkkcLnkDPskRpGsatakeil<-\*  
++ +++ r+p+ ++++++ +Ll + +n P+ Rp + e++  
sequence13 675 ADMAYHhIRPPIGYSIPKPISSLLIRGWNACPEGRP---EFSEV 716

Fig. 4B

```

gtcgcacccac gcgtccggtg aagggcagca gcacaggaga aaagcaaaga cttctttaa 60
atg ggg aat tac aaa tcc aga cca aca cag act tgt tct gat gaa tgg 108
Met Gly Asn Tyr Lys Ser Arg Pro Thr Gln Thr Cys Ser Asp Glu Trp
1 5 10 15
aag aag aaa gtt agt gaa tct tac gct att atc ata gaa agg ctg gag 156
Lys Lys Lys Val Ser Glu Ser Tyr Ala Ile Ile Ile Glu Arg Leu Glu
20 25 30
gat aac ctg cag atc aaa gaa aat gaa ttt caa gaa cta agg cac atc 204
Asp Asn Leu Gln Ile Lys Glu Asn Glu Phe Gln Glu Leu Arg His Ile
35 40 45
ttt ggc tct gat gaa gcc ttc agt gaa gtc agt tta aat tac cgc aca 252
Phe Gly Ser Asp Glu Ala Phe Ser Glu Val Ser Leu Asn Tyr Arg Thr
50 55 60
gag cgt ggc ctg tcc ctg cta cac ctc tgc tgt gtc tgt ggc ggc aac 300
Glu Arg Gly Leu Ser Leu Leu His Leu Cys Cys Val Cys Gly Gly Asn
65 70 75 80
aag tca cat atc cgt gcc ctt atg tta aaa ggg ctc cgt cca tcc aga 348
Lys Ser His Ile Arg Ala Leu Met Leu Lys Gly Leu Arg Pro Ser Arg
85 90 95
ctg acg aga aat ggg ttt cca gct ctg cac ctg gcc gtt tac aag gac 396
Leu Thr Arg Asn Gly Phe Pro Ala Leu His Leu Ala Val Tyr Lys Asp
100 105 110
agc ccg gaa ctt atc act tca ctg ttg cac agc gga gca gat gtt cag 444
Ser Pro Glu Leu Ile Thr Ser Leu Leu His Ser Gly Ala Asp Val Gln
115 120 125
caa gtg gga tac ggt ggc ctc aca gcc ctc cac ata gct gca ata gct 492
Gln Val Gly Tyr Gly Gly Leu Thr Ala Leu His Ile Ala Ala Ile Ala
130 135 140
gga cac cca gag gct gca gaa gtg ctg cta caa cat ggg gcc aat gtg 540
Gly His Pro Glu Ala Ala Glu Val Leu Leu Gln His Gly Ala Asn Val
145 150 155 160
aat gtt caa gat gcc gtc ttc ttc acc cca ctg cac att gca gcc tac 588
Asn Val Gln Asp Ala Val Phe Phe Thr Pro Leu His Ile Ala Ala Tyr
165 170 175
tat ggg cac gag cag gta acc agt gtc ctt ttg aag ttt ggt gct gat 636
Tyr Gly His Glu Gln Val Thr Ser Val Leu Leu Lys Phe Gly Ala Aspp
180 185 190
gtc aat gta agc ggt gaa gtt ggg gac agg cct ctg cac ctg gcc tct 684
Val Asn Val Ser Gly Glu Val Gly Asp Arg Pro Leu His Leu Ala Ser
195 200 205

```

Fig. 5A

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gca aag ggc ttc ttc aac att gtg aaa ctc ctg gta gaa gaa ggg agc	732
Ala Lys Gly Phe Phe Asn Ile Val Lys Leu Leu Val Glu Glu Gly Ser	
210 215 220	
aaa gca gat gtg aac gct cag gac aat gaa gac cac gtc cct ctg cac	780
Lys Ala Asp Val Asn Ala Gln Asp Asn Glu Asp His Val Pro Leu His	
225 230 235 240	
ttc tgt tct cga ttt gga cac cac aat ata gtg agc tac ctg ctc cag	828
Phe Cys Ser Arg Phe Gly His His Asn Ile Val Ser Tyr Leu Leu Gln	
245 250 255	
agt gac tta gag gtc cag cct cac gtc att aac atc tat ggt gac act	876
Ser Asp Leu Glu Val Gln Pro His Val Ile Asn Ile Tyr Gly Asp Thr	
260 265 270	
cct ttg cac ctg gca tgc tac aat gga aat ttt gaa gtt gcc aag gaa	924
Pro Leu His Leu Ala Cys Tyr Asn Gly Asn Phe Glu Val Ala Lys Glu	
275 280 285	
att gtc cag gta aca gga act gaa agt ctg act aag gaa aac atc ttc	972
Ile Val Gln Val Thr Gly Thr Glu Ser Leu Thr Lys Glu Asn Ile Phe	
290 295 300	
agc gag aca gct ttt cac agt gct tgt acc tat ggc aag aac att gac	1020
Ser Glu Thr Ala Phe His Ser Ala Cys Thr Tyr Gly Lys Asn Ile Asp	
305 310 315 320	
ctg gtc aaa ttt ctt ctt gat cag aat gct gtg aac att aac cac cga	1068
Leu Val Lys Phe Leu Leu Asp Gln Asn Ala Val Asn Ile Asn His Arg	
325 330 335	
gga aga gat ggg cac aca gga ttg cac tct gct tgc tac cac ggc cat	1116
Gly Arg Asp Gly His Thr Gly Leu His Ser Ala Cys Tyr His Gly His	
340 345 350	
atc cgc ctg gtt cag ttc cta ctt gat aat ggt gca gat atg aat ctt	1164
Ile Arg Leu Val Gln Phe Leu Leu Asp Asn Gly Ala Asp Met Asn Leu	
355 360 365	
gtc gct tgt gat ccc agc agg tct agt ggt gaa aaa gat gag cag aca	1212
Val Ala Cys Asp Pro Ser Arg Ser Ser Gly Glu Lys Asp Glu Gln Thr	
370 375 380	
tgt ttg atg tgg gct tac gag aaa gga cat gat gcc att gtt aca ctc	1260
Cys Leu Met Trp Ala Tyr Glu Lys Gly His Asp Ala Ile Val Thr Leu	
385 390 395 400	
ctg aag cac tac aag aga ccc cag gag gag ctg cca tgt aac gaa tat	1308
Leu Lys His Tyr Lys Arg Pro Gln Glu Glu Leu Pro Cys Asn Glu Tyr	
405 410 415	
tcc cag cct gga gga gat ggc tcc tat gtg tct gtt cct tcc ccc ttg	1356
Ser Gln Pro Gly Gly Asp Gly Ser Tyr Val Ser Val Pro Ser Pro Leu	
420 425 430	

Fig. 5B

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ggc aag att aaa agc atg aca aaa gag aag gca gat gtt ctc ctc ctg	1404
Gly Lys Ile Lys Ser Met Thr Lys Glu Lys Ala Asp Val Leu Leu Leu	
435 440 445	
agg gct gaa cta ccc tcc cgc ttc cat ctc caa ctc tcc gaa atc gag	1452
Arg Ala Glu Leu Pro Ser Arg Phe His Leu Gln Leu Ser Glu Ile Glu	
450 455 460	
ttc cac gag att atc ggc tgc ggt tcc ttt ggg aaa gtc tat aaa ggg	1500
Phe His Glu Ile Ile Gly Ser Gly Ser Phe Gly Lys Val Tyr Lys Gly	
465 470 475 480	
cga tgc aga aat aaa ata gtg gcg atc aaa cga tac cga gcc aac acc	1548
Arg Cys Arg Asn Lys Ile Val Ala Ile Lys Arg Tyr Arg Ala Asn The	
485 490 495	
tac tgc tcc aag tca gac gtg gat atg ttt tgc cga gag gtg tcc att	1596
Tyr Cys Ser Lys Ser Asp Val Asp Met Phe Cys Arg Glu Val Ser Ile	
500 505 510	
ctc tgc cag ctc aac cac ccc tgc gtg gtt cag ttt gtg ggt gcc tgc	1644
Leu Cys Gln Leu Asn His Pro Cys Val Val Gln Phe Val Gly Ala Cys	
515 520 525	
ctg gat gac ccc agt cag ttt gcc att gtc act cag tac att tca gga	1692
Leu Asp Asp Pro Ser Gln Phe Ala Ile Val Thr Gln Tyr Ile Ser Gly	
530 535 540	
ggc tcc ctg ttc tcc ctg ctt cat gaa cag aag aga att ctt gac ttg	1740
Gly Ser Leu Phe Ser Leu Leu His Glu Gln Lys Arg Ile Leu Asp Leu	
545 550 555 560	
cag tct aaa tta atc att gcg gta gac gtt gcc aag ggc atg gag tac	1788
Gln Ser Lys Leu Ile Ile Ala Val Asp Val Ala Lys Gly Mey Glu Tyr	
565 570 575	
ctg cac agc ttg acc cag cca atc ata cac cgc gac ctg aac agc cac	1836
Leu His Ser Leu Thr Gln Pro Ile Ile His Arg Asp Leu Asn Ser His	
580 585 590	
aat att ctg ctc tat gag gat ggc cat gct gtg gtg gca gat ttt gga	1884
Asn Ile Leu Leu Tyr Glu Asp Gly His Ala Val Val Ala Asp Phe Gly	
595 600 605	
gaa tca aga ttt ctg cag tcc ctg gat gaa gac aac atg aca aag cag	1932
Glu Ser Arg Phe Leu Gln Ser Leu Asp Glu Asp Asn Met Thr Lys Gln	
610 615 620	
cca ggg aac ctg cgc tgg atg gcc cct gag gtg ttc aca cag tgc acg	1980
Pro Gly Asn Leu Arg Trp Met Ala Pro Glu Val Phe Thr Gln Cys Thr	
625 630 635 640	
aga tac acc atc aag gct gat gtc ttc agt tac tcc ctg tgt ctg tgg	2028
Arg Tyr Thr Ile Lys Ala Asp Val Phe Ser Tyr Ser Leu Cys Leu Trp	
645 650 655	

Fig. 5C

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gag ctc ctc act gga gaa att cca ttc gct cat ctc aag cca gcc gct	2076
Glu Leu Leu Thr Gly Glu Ile Pro Phe Ala His Leu Lys Pro Ala Ala	
660 665 670	
gca gca gca gat atg gcg tat cac cac atc aga ccg ccc atc ggc tat	2124
Ala Ala Ala Asp Met Ala Tyr His His Ile Arg Pro Pro Ile Gly Tyr	
675 680 685	
tcc atc ccc aag ccc atc tca tcc ctg ctg ata ccg ggc tgg aat gca	2172
Ser Ile Pro Lys Pro Ile Ser Ser Leu Leu Ile Arg Gly Trp Asn Ala	
690 695 700	
tgt cct gaa gga cga cca gag ttc tct gaa gtc gtt agc aaa ctg gag	2220
Cys Pro Glu Gly Arg Pro Glu Phe Ser Glu Val Val Ser Lys Leu Glu	
705 710 715 720	
gag tgc cta tgc aat gtg gag ctc atg tct cca gca tca agt aac agc	2268
Glu Cys Leu Cys Asn Val Glu Leu Met Ser Pro Ala Ser Ser Asn Ser	
725 730 735	
agt ggc tct ctg tca cct tcc tct tct tcc gat tgc ctg ctg agc cgg	2316
Ser Gly Ser Leu Ser Pro Ser Ser Ser Ser Asp Cys Leu Leu Ser Arg	
740 745 750	
gga ggg cct ggc cgg agc cac gtg gca gcc tta ccg agc cgt ttt gag	2364
Gly Gly Pro Gly Arg Ser His Val Ala Ala Leu Arg Ser Arg Phe Glu	
755 760 765	
ttg gag tat gcc cta aat gca agg tcc tat gct ggg tgg tcc caa agt	2412
Leu Glu Tyr Ala Leu Asn Ala Arg Ser Tyr Ala Gly Trp Ser Gln Ser	
770 775 780	
gtt gga aca cac tct aat ccg ggc ctg tct ttg gag gag atg aat agg	2460
Val Gly Thr His Ser Asn Pro Gly Leu Ser Leu Glu Glu Met Asn Arg	
785 790 795 800	
agc acc cag tat tca act gtt gac aaa tac ggc tat gtg tct gat ccc	2508
Ser Thr Gln Tyr Ser Thr Val Asp Lys Tyr Gly Tyr Val Ser Asp Pro	
805 810 815	
atg agc ctg acg cac ctt cac tcc cgc caa gac gac agc aac ttt gag	2556
Met Ser Leu Thr His Leu His Ser Arg Gln Asp Asp Ser Asn Phe Glu	
820 825 830	
gac agc aac tgacaggtct ggcatacacc taaggggcgt ctcccatca	2605
Asp Ser Asn	
835	
ggctgacagc agtgatttta cccatggcag gcttgcttcc aattataacg ccctgccctc	2665
tgagggtttct tcaaatcgtc ttgcttattc taagctcggt taattccctt ctacaggaca	2725
ggctttgact catgccaaagc ctgaagtgtc aaagagcaga tacagaatgt gcatgaggaa	2785
ttgttcttag tttgatattt aaagccctta attgcctggg gctgggggttc aaatctgtgt	2845
agatagctgg gttgaccctt atgtatttgt agaccaaact gtgtgggctt gtgtttgagg	2905
gtctcctgtt gggtttctta aaaacaagct ggctgattta tctcctgttg cctttgttgt	2965
tacttctgtg attaaagtct cttcggtgat ctagaaaaaa aaaaaaaaaa agggcggccg	3025
c	3026

Fig. 5D

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Searching for complete domains in PFAM  
 hmmpfam - search a single seq against HMM database  
 HMMER 2.1.1 (Dec 1998)  
 Copyright (C) 1992-1998 Washington University School of Medicine  
 HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam4.4/Pfam  
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.11086.seq

Query: ratCARKpro

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
ank	Ank repeat	212.7	5.5e-60	9
pkinase	Eukaryotic protein kinase domain	206.4	4.3e-58	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
ank	1/9	66	99	1	33	1.2	48
ank	2/9	100	132	1	33	28.6	0.00014
ank	3/9	133	165	1	33	49.2	9.1e-11
ank	4/9	168	198	1	33	31.9	1.4e-05
ank	5/9	199	233	1	33	28.4	0.00017
ank	6/9	234	264	1	33	12.6	2.4
ank	7/9	269	302	1	33	23.1	0.0064
ank	8/9	306	338	1	33	11.2	3.5
ank	9/9	339	371	1	33	36.4	6.5e-07
pkinase	1/1	463	716	1	273	206.4	4.3e-58

Alignments of top-scoring domains:

ank: domain 1 of 9, from 66 to 99: score 1.2, E = 48

```

      *->nGnTPLHlAaryg.nvevvklLLehGAdvnartk<-*
      +G++ LHL++ g+n + +++L+ +G + t+
  ratCARKpro  66  RGLSLHLCCVCGgNKSHIRALMLKGLRPSRLTR  99
  
```

ank: domain 2 of 9, from 100 to 132: score 28.6, E = 0.00014

```

      *->nGnTPLHlAarygnvevvklLLehGAdvnartk<-*
      nG+ +LHLA++++ e++ LL GAdv + +
  ratCARKpro  100  NGFPALHLAVYKDSPELITSLHSGADVQQVG  132
  
```

ank: domain 3 of 9, from 133 to 165: score 49.2, E = 9.1e-11

```

      *->nGnTPLHlAarygnvevvklLLehGAdvnartk<-*
      G+T+LH+Aa++g+ e +++LL+hGA+vn+++
  ratCARKpro  133  GGLTALHIAAIAGHPEAAEVLLQHGANVNVQDA  165
  
```

ank: domain 4 of 9, from 168 to 198: score 31.9, E = 1.4e-05

```

      *->nGnTPLHlAarygnvevvklLLehGAdvnartk<-*
      +TPLH+Aa+yg+ +v +LL+ GAdvn+ +
  ratCARKpro  168  --FTPLHIAAYYGHEQVTSVLLKFGADVNVSGE  198
  
```

ank: domain 5 of 9, from 199 to 233: score 28.4, E = 0.00017

```

      *->nGnTPLHlAarygnvevvklLLe..hGAdvnartk<-*
      G+ PLHLA+ +g ++vklL+e++ Advna+++
  ratCARKpro  199  VGDRPLHLASAKGFFNIVKLLVEegSKADVNAQDN  233
  
```

Fig. 6A

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```

ank: domain 6 of 9, from 234 to 264: score 12.6, E = 2.4
      *->nGnTPLHlAarygnvevkvllLehGAdvnartk<-*
      + PLH ++r g+ ++v +LL+ +d ++
ratCARKpro 234 EDHVPLHFCSRFQHHNIVSYLLQ--SDLEVQPH 264

ank: domain 7 of 9, from 269 to 302: score 23.1, E = 0.0064
      *->nGnTPLHlAarygnvevkvllLe.hGAdvnartk<-*
      G+TPLHlA+++gn ev+k ++ G+ + +
ratCARKpro 269 YGDTPLHLACYNGNFEVAKEIVQvTGTESLTEN 302

ank: domain 8 of 9, from 306 to 338: score 11.2, E = 3.5
      *->nGnTPLHlAatyg.nvevkvllLe.hGAdvnartk<-*
      T+ H A+ yg+n+++vk+LL+++ ++n r +
ratCARKpro 306 --ETAFHSACTYgkNIDLVKFLLDqNAVNIHRGR 338

ank: domain 9 of 9, from 339 to 371: score 36.4, E = 6.5e-07
      *->nGnTPLHlAarygnvevkvllLehGAdvnartk<-*
      +G+T LH A+++g++++v++LL++GAd n +
ratCARKpro 339 DGHTGLHSACYHGHIRLVQFLLDNGADMNLVAC 371

pkinase: domain 1 of 1, from 463 to 716: score 206.4, E = 4.3e-58
      *->yelleklGeGsfgkVykakhtgkivAvKilk.....kesls..lr
      +e+++G+GsfgkVyk++ + +kivA+K + ++ +k++++ r
ratCARKpro 463 IEFHEIIIGSGSFGKVYKGRCR-NKIVAIAKRYRantycsKSDVDmfCR 508

      EiqilkrslsHpNIvrllgvfedtdhlylvmEymegGdLfdylrrng.pl
      E++il +l+Hp +v++ g++ d+++ + +v++y gG+lf++l+++++ l
ratCARKpro 509 EVSILCQLNHPCVVQFVGACLDPSQFAIVTQYISGSLFSLLEHQRIL 558

      sekeakkialQilrGleYlHsng..ivHRDLKpeNIlldengtviKiaDFG
      + + + ia +++G+eYlHs ++i+HRDL + NIl e+g+ +aDFG
ratCARKpro 559 DLQSKLIIAVDVAKGMEYlHSLTqpIIHRDLNSHNILLYEDGHAVVADFG 608

      LArll.....eklttfvGtpwYmmAPEvileg.rgysskvDvWSlGviLy
      +r+l++ ++ ++t G +++m APEv + + y+ k+Dv S+ L+
ratCARKpro 609 ESRFLqsldeDNMTKQPGNLRWM-APEV-FTQcTRYTIKADVFSYSLCLW 656

      ElltggplfpgadlpafgtggdevdqliifvklPfsdelpktridpleel

      Elltg ++Pf + +p ++
ratCARKpro 657 ELLTG-----EIPFAH-----LKPAAAA 674

      frikkr..rlplpsncSeelkdLlkkcLnkDPskRpGsatakeil<-*
      ++ +++ r+p+ +++++ +Ll + +n P+ Rp + e++
ratCARKpro 675 ADMAYHhirPPIGYSIPKPISSLLIRGWNACPEGRP---EFSEVV 716

```

Fig. 6B

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GAP of: AAAa006\_n check: 4956 from: 1 to: 3025

cark (analysis only) - Import - complete

to: BAAa006\_n check: 6389 from: 1 to: 3026

Rat CARK cDNA (analysis only) - Import - complete

Symbol comparison table: /ddm\_local/gcg/gcg\_9.1/gcgcore/data/rundata/  
 nwsgapdna.cmp

CompCheck: 8760

Gap Weight: 12 Average Match: 10.000  
 Length Weight: 4 Average Mismatch: 0.000

Quality: 24376 Length: 3045  
 Ratio: 8.058 Gaps: 14  
 Percent Similarity: 82.169 Percent Identity: 82.169

Match display thresholds for the alignment(s):

| = IDENTITY  
 : = 5  
 . = 1

AAAa006\_n x BAAa006\_n

```

      .               .               .               .
1  gtcgacccacgcgtccg.....gccctggagaaaggaagaaa 37  human
   |||||
1  GTCGACCCACGCGTCCGGTGAAGGGCAGCAGCACAGGAGAAAAGCAAAGA 50  rat
      .               .               .               .
38 cttataataaatgggaaattataaatctagaccaacccaaacttgactg 87
   |||||
51 CTTCTTTTAAATGGGGAATTACAAATCCAGACCAACACAGACTTGTCTG 100
      .               .               .               .
88 atgaatggaagaaaaaagtcagtgaatcatatggtatcacaatagaaaga 137
   |||||
101 ATGAATGGAAGAAGAAAGTTAGTGAATCTTACGCTATTATCATAGAAAGG 150
      .               .               .               .
138 ttagaagatgacctgcagatcaaggaaaaagaactgacagaactaaggaa 187
   |||||
151 CTGGAGGATAACCTGCAGATCAAAGAAAATGAATTTCAAGAACTAAGGCA 200
      .               .               .               .
188 tatatttggctctgatgaagccttcagtaaagtcaatttaaattaccgca 237
   |||||
201 CATCTTTGGCTCTGATGAAGCCTTCAGTGAAGTCAGTTTAAATTACCGCA 250
      .               .               .               .
238 ctgaaaatgggctgtctctacttcatttatgttgcatgttgagggaag 287
   |||||
251 CAGAGCGTGGCCTGTCCCTGCTACACCTCTGCTGTGTCTGTGGCGGCAAC 300

```

Fig. 7A

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```

      .           .           .
288 aaatcacatattcgaactcttatgttgaaagggctccgcccattctcgact 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 AAGTCACATATCCGTGCCCTTATGTTAAAAGGGCTCCGTCCATCCAGACT 350
      .           .           .
338 gacaagaaatggatttacagccttgcathtagcagtttacaaggataatg 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
351 GACGAGAAATGGGTTTCCAGCTCTGCACCTGGCCGTTTACAAGGACAGCC 400
      .           .           .
388 cagaattgatcacttctctgcttcacagtggagctgatatacagcaggtt 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
401 CGGAACTTATCACTTCACTGTTGCACAGCGGAGCAGATGTTTCAGCAAGTG 450
      .           .           .
438 ggatacgggtggcctcactgccctccatattgctacaatagctggccacct 487
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
451 GGATACGGTGGCCTCACAGCCCTCCACATAGCTGCAATAGCTGGACACCC 500
      .           .           .
488 agaggctgctgatgtgctgttgcaacatggagctaattgtcaatattcaag 537
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
501 AGAGGCTGCAGAAGTGCTGCTACAACATGGGGCCAATGTGAATGTTCAAG 550
      .           .           .
538 atgcagtttttttctcactccattgcatattgcagcgctactatggacatgaa 587
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
551 ATGCCGTCTTCTTCACCCCACTGCACATTGCAGCCTACTATGGGCACGAG 600
      .           .           .
588 caggtaactcgccttcttttgaaatttggtgctgatgtaaagtgaagtgg 637
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 CAGGTAACCAGTGTCTTTTGAAGTTTGGTGCTGATGTCAATGTAAGCGG 650
      .           .           .
638 tgaagttggagatagaccctccacctagcatctgcaaaaggattcttga 687
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
651 TGAAGTTGGGGACAGGCCTCTGCACCTGGCCTCTGCAAAGGGCTTCTTCA 700
      .           .           .
688 atattgcaaaactcttgatggaagaaggcagcaaagcagatgtgaatgct 737
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
701 ACATTGTGAAACTCCTGGTAGAAGAAGGGAGCAAAGCAGATGTGAACGCT 750
      .           .           .
738 caagataatgaagaccatgtcccactccatttctgttctcgatttggaca 787
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
751 CAGGACAATGAAGACCACGTCCCTCTGCACCTTCTGTTCTCGATTTGGACA 800
      .           .           .
788 ccatgatatagttaagtatctgctgcaaagtgatttggaagttcaacctc 837
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
801 CCACAATATAGTGAGCTACCTGCTCCAGAGTGACTTAGAGGTCCAGCCTC 850
      .           .           .
838 atgttgттаатatctatggagatacccccttacacctggcatgctacaat 887
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
851 ACGTCATTAACATCTATGGTGACACTCCTTTGCACCTGGCATGCTACAAT 900
      .           .           .
888 ggcaaatttgaaagttgccaaggaaatcatccaaatatcaggaacagaaag 937
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
901 GGAAATTTTGAAGTTGCCAAGGAAATTGTCCAGGTAACAGGAAGTGAAG 950

```

Fig. 7B

```

938 tctgactaaggaacacatcttcagtgaacagcttttcatagtgccttgta 987
    |||
951 TCTGACTAAGGAAAACATCTTCAGCGAGACAGCTTTTCACAGTGCTTGTA 1000
    |||
988 cctatggcaagagcattgacctagtcaaatttcttcttgatcagaatgtc 1037
    |||
1001 CCTATGGCAAGAACATTGACCTGGTCAAATTTCTTCTTGATCAGAATGCT 1050
    |||
1038 ataaacatcaaccaccaaggaagggatgggcacactggattacactctgc 1087
    |||
1051 GTGAACATTAACCACCGAGGAAGAGATGGGCACACAGGATTGCACTCTGC 1100
    |||
1088 ttgctaccacggtcacattcgcctgggttcagttcttactggataatggag 1137
    |||
1101 TTGCTACCACGGCCATATCCGCTGGTTCAGTTCCTACTTGATAATGGTG 1150
    |||
1138 ctgatatgaatctagtggcttgatcccagcaggtctagtggtgaaaaa 1187
    |||
1151 CAGATATGAATCTTGTCGCTTGATGCCAGCAGGTCTAGTGGTGAAAAA 1200
    |||
1188 gatgagcagacatgtttgatgtgggcttatgaaaaagggcatgatgccat 1237
    |||
1201 GATGAGCAGACATGTTTGATGTGGGCTTACGAGAAAGGACATGATGCCAT 1250
    |||
1238 tgtcacactcctgaagcattataagagaccacaagatgaattgccctgta 1287
    |||
1251 TGTTACACTCCTGAAGCACTACAAGAGACCCCAGGAGGAGCTGCCATGTA 1300
    |||
1288 atgaatattctcagcctggaggagatggctcctatgtgtctgttccatca 1337
    |||
1301 ACGAATATTCCCAGCCTGGAGGAGATGGCTCCTATGTGTCTGTTCTCTCC 1350
    |||
1338 cccttggggaagattaaaagcatgacaaaagagaaggcagatattctcct 1387
    |||
1351 CCCTTGGGCAAGATTAAAAGCATGACAAAAGAGAAGGCAGATGTTCTCCT 1400
    |||
1388 cctaagagctggattgccttcacatttccatcttcagctctcagaaattg 1437
    |||
1401 CCTGAGGGCTGAACTACCCTCCCGCTTCCATCTCCAACCTCTCCGAAATCG 1450
    |||
1438 agttccatgagattattggctcaggttcttttgggaaagtatataaagga 1487
    |||
1451 AGTTCCACGAGATTATCGGCTCGGGTTCCTTTGGGAAAGTCTATAAAGGG 1500
    |||
1488 cgatgcagaaataaaaatagtggctataaaacgttatcgagccaataccta 1537
    |||
1501 CGATGCAGAAATAAAATAGTGGCGATCAAACGATACCGAGCCAACACCTA 1550
    |||

```

Fig. 7C

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```
1538 ctgctccaagtcagatgtggatatgttttgccgagaggtgtccattctct 1587
      |||
1551 CTGCTCCAAGTCAGACGTGGATATGTTTTGCCGAGAGGTGTCCATTCTCT 1600
      |||
1588 gccagctcaatcatccctgcgtaattcagtttggtgggtgcttgcttgaat 1637
      |||
1601 GCCAGCTCAACCACCCCTGCGTGGTTCAGTTTGTGGGTGCCTGCCTGGAT 1650
      |||
1638 gatcccagccagtttgccattgtcactcaatacatatcagggggttctct 1687
      |||
1651 GACCCAGTCAGTTTGCCATTGTCACTCAGTACATTTTCAGGAGGCTCCCT 1700
      |||
1688 gttctccctccttcatgagcagaagaggattcttgatttgagtcctaaat 1737
      |||
1701 GTTCTCCCTGCTTCATGAACAGAAGAGAATTCTTGACTTGCAGTCTAAAT 1750
      |||
1738 taattattgcagtagatgttgccaaaggcatggagtaccttcacaacctg 1787
      |||
1751 TAATCATTGCGGTAGACGTTGCCAAGGGCATGGAGTACCTGCACAGCTTG 1800
      |||
1788 acacagccaattatacatcgtgacttgaacagtcacaatattcttctcta 1837
      |||
1801 ACCCAGCCAATCATACACCGCGACCTGAACAGCCACAATATTCTGCTCTA 1850
      |||
1838 tgaggatgggcatgctgtggtggcagatttttgagaatcaagatttctac 1887
      |||
1851 TGAGGATGGCCATGCTGTGGTGGCAGATTTTGAGAAATCAAGATTTCTGC 1900
      |||
1888 agtctctggatgaagacaacatgacaaaacaacctgggaacctccgttgg 1937
      |||
1901 AGTCCCTGGATGAAGACAACATGACAAAGCAGCCAGGGAACCTGCGCTGG 1950
      |||
1938 atggctcctgaggtgttcacgcagtgactcggtacaccatcaaagcaga 1987
      |||
1951 ATGGCCCCCTGAGGTGTTACACAGTGCACGAGATACACCATCAAGGCTGA 2000
      |||
1988 tgtcttcagctatgctctgtgtctgtgggaaattctcactggcgaaattc 2037
      |||
2001 TGTCTTCAGTTACTCCCTGTGTCTGTGGGAGCTCCTCACTGGAGAAATTC 2050
      |||
2038 cattcgctcatctcaagccagcggctgcggcagcagacatggcttaccac 2087
      |||
2051 CATTCGCTCATCTCAAGCCAGCCGCTGCAGCAGCAGATATGGCGTATCAC 2100
      |||
2088 cacatcagacctccattggctattccattcccaagcccatatcatctct 2137
      |||
2101 CACATCAGACCGCCCATCGGCTATTCCATCCCAAGCCCATCTCATCCCT 2150
      |||
2138 gctgatacgaggggtggaacgcagtcctgaaggaagacccgaattttctg 2187
      |||
2151 GCTGATACGGGGCTGGAATGCATGTCTCTGAAGGACGACCAGAGTCTCTG 2200
```

Fig. 7D

Fig. 7E

```
2787 ttttgtaaattaaaaaaaaatttagatcggttacttggaaatggagcctaa 2836
    ||| ||| | ||| ||| ||| ||| ||| ||| ||| |||
2796 TTTGATATTT....AAAGCCCTTA....ATTGCCTGGGGCTGGGGTTCAA 2837
    .
2837 gtctgtggtggaca.....gataataattatgttttcctgggctgaatta 2881
    ||||| ||| ||| | ||| ||| ||| ||| ||| ||| |||
2838 ATCTGT.GTAGATAGCTGGGTTGACCCTTATGTATTTGTAGACCAAACCTG 2886
    .
2882 tgtagacttgtgtttgacag.ctatggggtttatcttcttagaacattgttc 2930
    ||| | ||||| ||||| ||| ||| ||| ||| ||| ||| |||
2887 TGTGGGCTTGTGTTTGAGGGTCTCCTGTTGGGTTTCTTAAAAACAAGCTG 2936
    .
2931 attttcttttctcattatgttacttctagtgttcacctctgtgattaaag 2980
    | ||| |||| | |||| | ||| ||| ||| ||| ||| ||| |||
2937 GCTGATTTATCTC...CTGTTGCCTTTGTGTT.ACTTCTGTGATTAAAG 2982
    .
2981 attctttggtgaaatagaaaaaaaaaaaaaaaaaagggcgccgc 3025
    |||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
2983 TCTCTTCGGTGATCTAG.AAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3026
```

Fig. 7F

GAP of: IAAa006\_n check: 1490 from: 1 to: 836

ratCARKpro (analysis only) - Import - complete

to: JAAa006\_n check: 4709 from: 1 to: 835

carkprot (analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/B:AST/matrix/aa/BLOSUM62

CompCheck: 1102

Matrix made by matblas from blosum62.ii

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248
Quality:	4079	Length:	836
Ratio:	4.885	Gaps:	0
Percent Similarity:	93.174	Percent Identity:	91.377

Match display thresholds for the alignment(s):

| = IDENTITY  
 : = 2  
 . = 1

IAAa006\_n x JAAa006\_n

1	MGNYSRPTQTCSDEWKKKVSESYAIIIERLEDNLQIKENEFQELRHIFG	50	rat
1	MGNYSRPTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELNRNIFG	50	human
51	SDEAFSEVSLNYRTERGLSLLHLCCVCGGNKSHIRALMLKGLRPSRLTRN	100	
51	SDEAFSKVNLNYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRN	100	
101	GFPALHLAVYKDSPELITSLHSGADVQVQVGYGGLTALHIAAIAGHPEAA	150	
101	GFTALHLAVYKDNAELITSLHSGADIQVQVGYGGLTALHIATIAGHLEAA	150	
151	EVLLQHGANGVNVQDAVFFTPLHIAAAYYGHEQVTSVLLKFGADVNVSGEVG	200	
151	DVLLQHGANGVNIQDAVFFTPLHIAAAYYGHEQVTRLLLKFGADVNVSGEVG	200	
201	DRPLHLASAKGFFNIVKLLVEEGSKADVNAQDNEDHVPLHFCSRFGHHNI	250	
201	DRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVPLHFCSRFGHHDI	250	
251	VSYLLQSDLEVQPHVINIYGDTPHLACYNNGFEVAKEIVQVTGTESLTK	300	
251	VKYLQSDLEVQPHVVNIYGDTPHLACYNKFEVAKEIIQISGTESLTK	300	

Fig. 8A

```

301 ENIFSETAFHSACTYGKNIDLKFLLDQNAVNNINHRGRDGHTGLHSACYH 350
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQGRDGHTGLHSACYH 350
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
351 GHIRLVQFLLDNGADMNLVACDPSRSSGEKDEQTCLMWAYEKGHDAIVTL 400
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
351 GHIRLVQFLLDNGADMNLVACDPSRSSGEKDEQTCLMWAYEKGHDAIVTL 400
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
401 LKHYKRPQEELPCNEYSQPGGDGSYVSVPSPLGKIKSMTKEKADVLLLR 450
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
401 LKHYKRPQDELPCNEYSQPGGDGSYVSVPSPLGKIKSMTKEKADILLR 450
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
451 ELPSRFHLQLSEIEFHEIIGSGSFGKVYKGRCRNKIVAIKRYRANTYCSK 500
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
451 GLPSHFHLQLSEIEFHEIIGSGSFGKVYKGRCRNKIVAIKRYRANTYCSK 500
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
501 SDVDMFCREVSILCQLNHPCVVQFVGACLDPSQFAIVTQYISGGSLSL 550
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
501 SDVDMFCREVSILCQLNHPCVIQFVGACLDPSQFAIVTQYISGGSLSL 550
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
551 LHEQKRILDQLSKLIIAVDVAKGMEYLHSLTQPIIHRDLNSHNILLYEDG 600
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
551 LHEQKRILDQLSKLIIAVDVAKGMEYLHNLTPQPIIHRDLNSHNILLYEDG 600
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
601 HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFS 650
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
601 HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFS 650
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
651 YSLCLWELLTGEIPFAHLKPAAAAADMAYHHIRPPIGYSIPKPISSLLIR 700
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
651 YALCLWEILTGEIPFAHLKPAAAAADMAYHHIRPPIGYSIPKPISSLLIR 700
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
701 GWNACPEGRPEFSEVVSKLEECLCNVELMSPASSNSSGSLSPSSSSDCLL 750
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
701 GWNACPEGRPEFSEVVMKLEECLCNIELMSPASSNSSGSLSPSSSSDCLV 750
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
751 SRGGPGRSHVAALRSRFELEYALNARSYAGWSQSVGTHSNPGLSLEEMNR 800
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
751 NRGGPGRSHVAALRSRFELEYALNARSYAALSQAGQYSSQGLSLEEMKR 800
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
801 STQYSTVDKYGYSVDPMSLTHLSRQDDSNFEDSNX 836
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
801 SLQYTPIDKYGYSVDPMSMHHFHSRNSSSSFEDSS. 835
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Fig. 8B

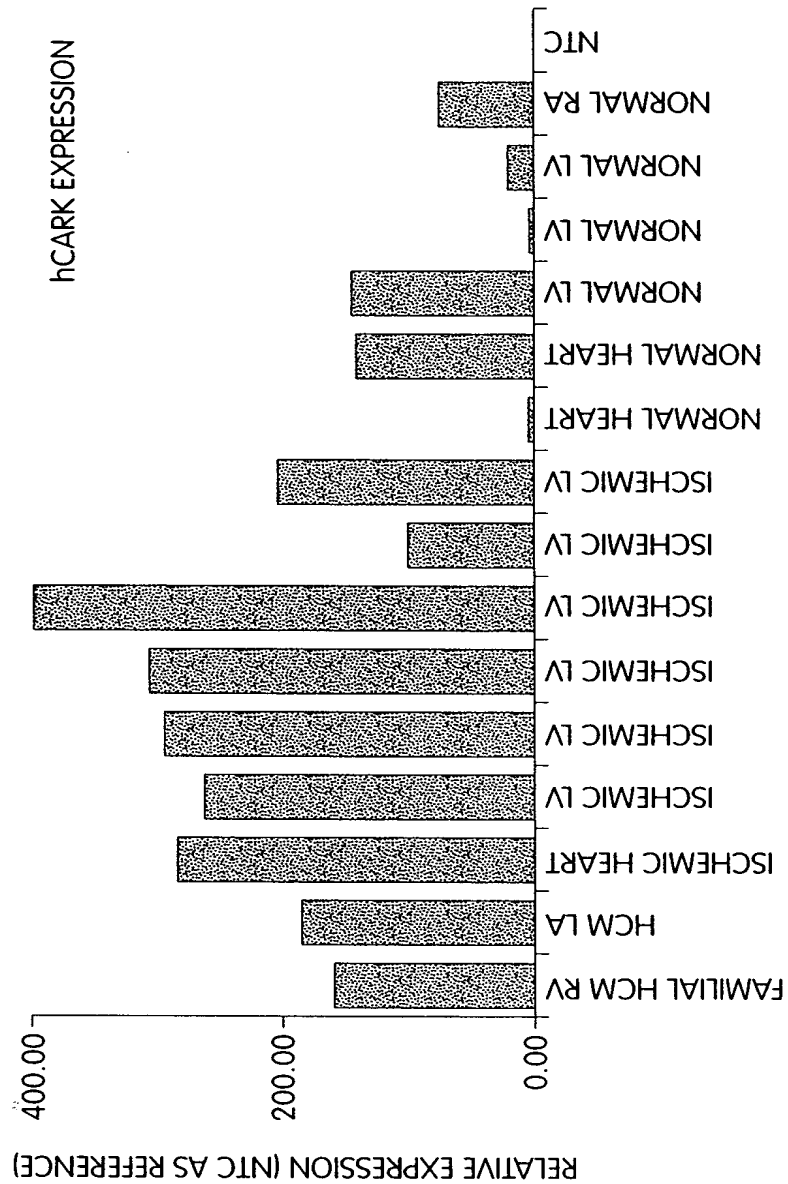


Fig. 9

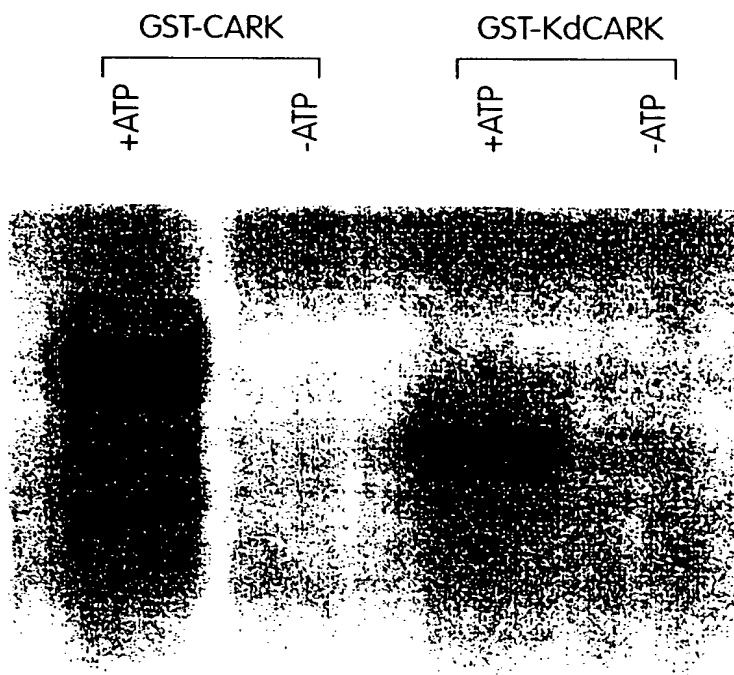


Fig. 10

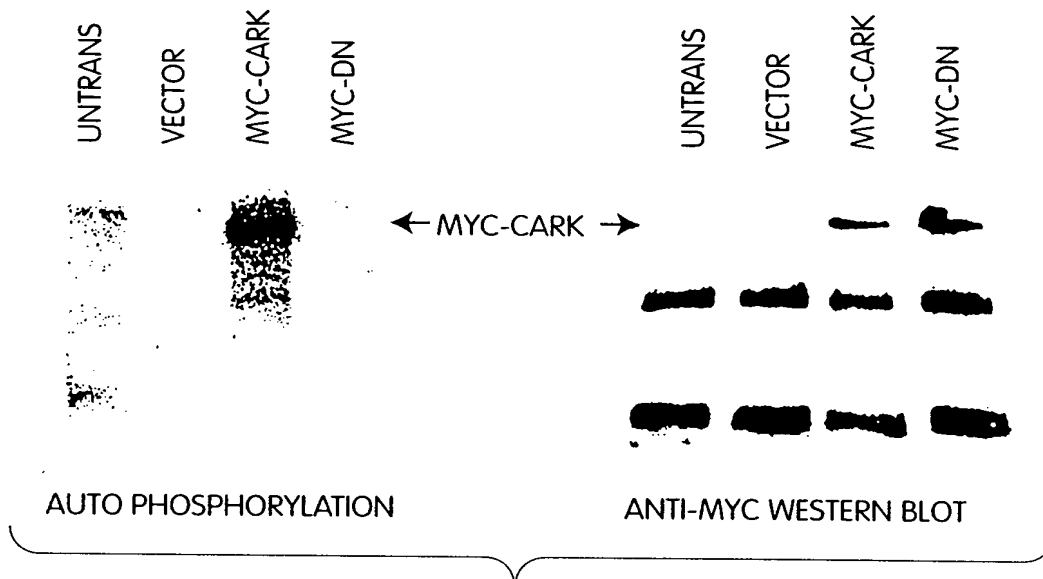


Fig. 11

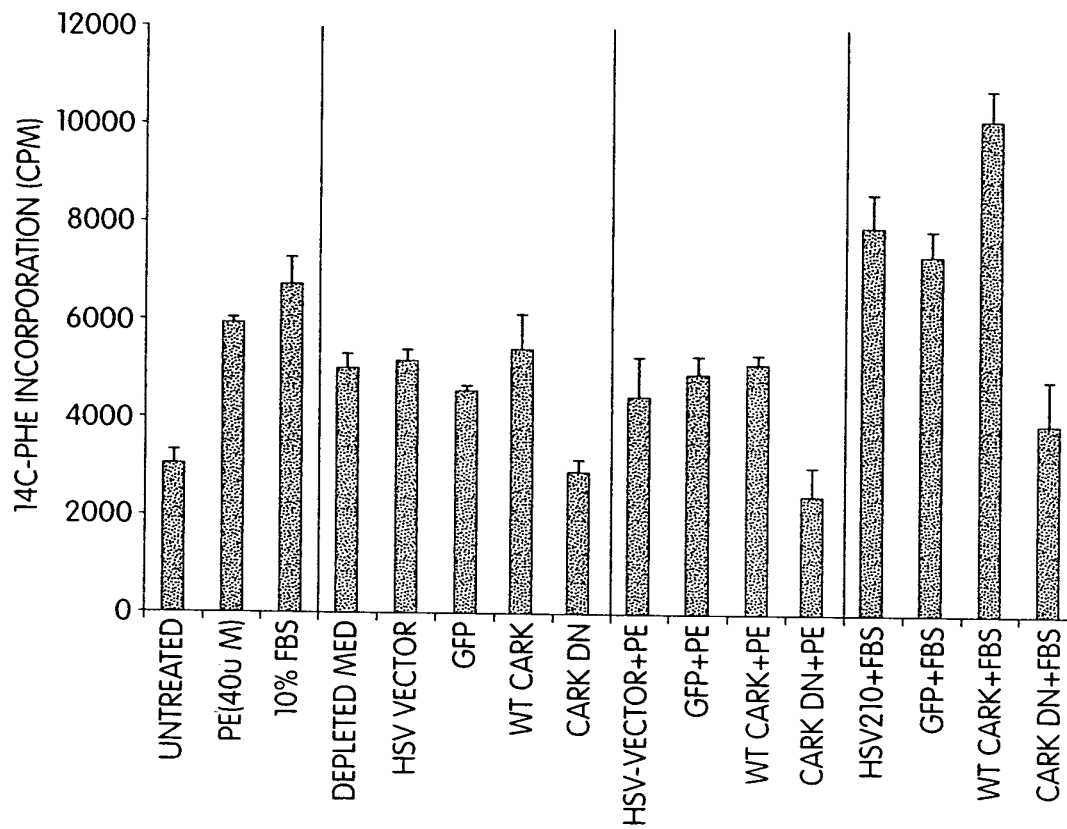


Fig. 12